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Title:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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37.2	37.2	37.5	38.1	38.1	38.4	38.9	39.7	40.5	64.3	77.6	77.6	82.6	91.1	91.4	92.6	94.5	97.3	100.0	Query Match
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344	346.6	364.2	364.2	364.2	389	393.8	393.8	393.8	393.8	426.2	427.2	430.4	436.2	444.8	445.4	447.6	449.2	449.6	449.6	450.6	451	453.2	453.2	455.6	455.6
28.0		29.6	29.6	29.6	31.6	32.0	32.0	32.0	32.0	34.7	34.7	35.0	35.5	36.2	36.2	36.4	36.5	36.6	36.6	36.6	36.7	36.8	36.8	37.0	37.0
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ALIGNMENTS

	CDS	gene	SOUTOR	FEATURES	JOURNAL	TITLE	AUTHORS	JOURNAL	TITLE	REFERENCE	SOURCE ORGANISM	RESULT 1 AF083913 LOCUS DEFINITION ACCESSION VERSION KEYWORDS
/gene="AnnAtl" /note="calcium-binding protein" /codon_start=1 /codon_start=1 /product="annexin" /product="annexin" /protein_id="AAD34236.1" /protein_id="AAD34236.1" /db_xref="G1:4959106" /db_xref="G1:4959106" /translation="MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAE /translation="MATLKTLDKELSNDFERALILAWTLEPGERDALLANEATKRWTSS QRKVIRQAYHETYGEDLLKTLDKELSNDFERALILAWTLEPGGREDALLANEATKRWTSS NQULMENGATRISTYGLLHARGAYKSSLEEDVAHHTTGDFKKLLVSLVTSYRYEG DEVNMTLAKQEAKLVHEKIKDKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILK SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID	34. 987	/mol_type="mRNA" /cultivar="Columbia" /db_xref="taxon:3702" 1.	/organism="Arabidopsis thaliana"		Submitted (12-AUG-1998) Botany, University of Texas, 24th at Whitis, Austin, TX 78713, USA	Direct Submission	Clark, G.B. and Roux, S.J.	CUMNS (ACCESSION NOS. AF083913 data AF083914) (FGK 99-083) Plant Physical 1220 (1), 340 (1999)		Spermatophyta; Magnoliophyta; educiotylegilyra; Educatylyra; Spermatophyta; Magnoliophyta; educiotylegilyra; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1230)	Arabidopsis thaliana (thale cress) Arabidopsis thaliana	AF083913 1230 bp mRNA linear PLN 02-JUN-1999 Arabidopsis thaliana annexin (AnnAt1) mRNA, complete cds. AF083913 AF083913.1 GI:4959105

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                                                                                                                                                                               Nguyen, M, (SSP/
equally to this
(SSP/Stanford)
                                                                                                                                                                                                                                       The Salk, Stanford, PGEC (SSP) Consortium members carried out th sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamadda,K., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                              collection and clustering of RAFL cDNAs (RAFL cDNA; 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (02-JAN-2002) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nguyen,M., Karlin.Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1108)
Tractic Magnoliophyta;
Conthuick A Lam B Miranda M.
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                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Genomic Sciences Center (GSC) members carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                     e-mail for correspondence: arab@sequence.stanford.edu
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33. .986
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/chromosome="1"
/clone="RAFL06-11-P04"
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                           (SSP/Stanford) and Seki, M.
                                                                                                                                    organism="Arabidopsis
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                                                                                                                      type="mRNA"
                                                                                                                                                                              work. Shinozaki, K. contributed equally
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                                                                                                                                                                               (RIKEN GSC) contributed (RIKEN GSC) and Davis, R. to this work as PIs.
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PLN 20-JAN-2002

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TTGAGGTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGT
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Pred. No. 1.5e-292;
0; Mismatches 1;
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FEATURES	JOURNAL		JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	REFERENCE AUTHORS TITLE	RESULT 3 AYOB6570 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	Qy 11 Db 11	ΟΥ 10 Db 10	Οy 10 Db 10	Qy 9	Qy 9	Qy 8
this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the cereminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the full-length clones. Ceres, Inc. carried out the clustering of the Location/Qualifiers	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of	Full-Length cDNA from Arabidopsis thaliana Unpublished Joases 1 to 1192) Brover, V., Troukhan, M., Alexandrov, N., Lu, YP., Flavell, R. and Feldmann, K.	Genome Biol. 3 (6), RESEARCH0029 (2002) 22088475 12093376 2 (bases 1 to 1192) Brover, V., Troukhan, M., Alexandrov, N., Lu, YP., Flavell, R. and Feldmann, K.	ids II; Brassicales; Brassicaceae; Arco 1192) Co 1192) Difovsky,N., Town,C.D., Troukhan,M., A., Flavell,R.B., White,O. and Salzberg., Flavelr, R.B., white,O. and Salzberg.	AY086570 Arabidopsis thaliana clone 25846 mRNA, complete sequence. AY086570 AY086570.1 GI:21405280 FLI CDNA. Arabidopsis thaliana (thale cress) Arabidopsis thaliana (thale cress) Arabidopsis thaliana (thale cress) Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sparmarophyta, Maranoliophyta; endicotyledons; core endicots;	.50 GAGAGACAGAGAGAACCAGTGTGGTCTCTTAAGTTATATATA	.090 TTCTACAAAAACCTTGTTTGTTTCTGTTGTGTGTGTTTTGAGTTCCTAAATAATGCAAAAGA 1149 	030 TCTGTTATCTCTTATCTCCCTCTCTCTCTCTTTGATGAGTTTCAAATCGTTTGATTTTGT 1089	70 GGTGAAGATGATGCTTAATCAATCAATCCACAGAGAAACATAAGCTGCTCTACAGCT 1029 	910 GAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTC 969 	850 GCTGAGATTGACTTGAAGGTCATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTG 909

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Query Match
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SLEEGDDDDKFLALLRSTIQCLTRPELLYFVDVLRSAINKTGTDEGALTRIVTTRAEID
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36, .989
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Pred. No. 1.1e-283;
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                                                                BT003359 1139 bp mRNA linear E Arabidopsis thaliana Ca2+-dependent membrane-binding annexin (At1g35720) mRNA, complete cds.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                              CDNA.
                                          GI:28059005
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collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                       Southwick, A., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T., Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Lee, J.M., Ishida, J., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Onodera, C.S., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shinn, P., Tang, C.C., Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission

Submitted (29-JAN-2003) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1139)
                                                                                                                                                                                                                                                              e-mail
                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                              correspondence: arab@sequence.stanford.edu
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFT CDNAs: Nguyen, M., Tripp, M., Southwick, A., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Kim, C.J., Quach, H.L., Onodera, C.S., Shinn, P., Tang, C.C., Kim, C.J., Quach, H.L., Onodera, C.S., Shinn, P., Tang, C.C., Kim, C.J., Quach, H.L., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Ecker, J., Thomas, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Ecker, J., Thomas, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Ecker, J., Theologis, A. and Davis, R.W.

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TTGAGGTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGT

Nguyen,M., (SSP/Stan: equally to this work. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.

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                                                                                                                      GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
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      ATCAATGCTACTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAGTCTT
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                                                      GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
                                                                                                 GATGAAGTGAACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
                                                                                                                                                                ACTACCGGTGACTTCAGAAAGCTTTTGGTTTCTCTTTACCTCATACAGGTACGAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Ca2+-dependent membrane-binding protein annexin"
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/protein_id="AA029977.1"
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LKVIGEEYQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ecotype="Columbia"
/note="This clone is in
PCR product using RIKEN
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db_xref="taxon:3702"
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Pred. No. 9.7e-278;
); Mismatches 0;
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheo;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
rosids, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Strasbourg, FRANCE
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A.thaliana mRNA
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                                                                                                                             /sub_species="ecotype
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/clone="FAFM80"
                                                                               function="calcium"
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EEGDDDDKFLALLRSTIGCLTRFELFYDVLRSAINKTGTDEGALTRIVTTRAEIDLK
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Gidrol, X., Sabelli, P.A., Fern, Y.S. and Kush, A.K.
Annexin-like protein from Arabidopsis thaliana reso
mutant of Escherichia coli from H202 stress
Proc. Natl. Acad. Sci. U.S.A. 93 (20), 11268-11273
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Arabidopsis thaliana
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Eukaryotopis Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Direct Submission
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QRKVIRQAYHETYGKDLKKILDKELSNDFBRAILLWTLEPGERDALLANEATKWTSS
QQYLMEVACTRTSTQLLHARQAYHARYKKSLEEDHAHTTGDFRKLLVSLVTSYRYEG
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SLEEGDDDDKLPCTLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID
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/db_xref="taxon:3702"
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Query Match
Best Local Similarity
Matches 1149; Conserv

Conservative

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91.1%;

Score 1120; Pred. No. 6.

.4e-273; DB

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Length 1159; Indels

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                                     CCCTCTCTCTCTTGATGAGTTTCAAATCGTTTGATTTTGTTTCTACAAAAACCTTGTTT
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                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-JUN-2000) Plant Gene Expression Center, 800 Buchanan St., Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced gi:6693723.
The sequence is of BAC F14D7 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 6954 by because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide small overlaps (200 bp) between overlapping sumbitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 81513)

Liu,S.X., Chan,A., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Toriumi,M., Chin,C., Chiou,J., Choi,E., Chang,M., Gonzalez,A., Howng,B., Liu,A., Vaysberg,M., Altafi,H., Brooke,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Klan,S., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A., Theologis,A. and Yu,G.

The sequence of BAC F14D7 from Arabidopsis thaliana chromosome 1
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complete
AC021198
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Submitted (15-JAN-2000) P.
Street, Albany, CA 94710,
3 (bases 1 to 81513)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-FEB-2000)
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/clone="F14D7"
1553. .4999
/gene="Fi4D7.1"
join(1553. .4628,4713. .4999)
join(1553. .4628,4713. .4999)
/gene="F14D7.1"
/gene="Contains similarity to receptor protein kinase-like
/note="Contains similarity to receptor protein kinase-like
/note="Contains a eukaryotic protein kinase domain pF|00069. EST
gb|AI997574 comes from this gene."
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                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/mol_type="genomic_DNA"
/cultivar="Columbia"
                                                                                                                                                                                                                        db_xref="taxon:3702"
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misc_feature
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LSQNKLTGS I PSSLGNLKNLTLLSLFQNYLTGG I PSKLGNLKNLTGSI
PSSLGNLKNLT ILVIENYLTGVI PPELGNMESMI DLELSNNKLTGSI
PSSLGNLKNLT ILVIENYLTGVI PPELGNMESMI DLOLUNNIKLTGS I PSSFGNLKNL
TYLYLYLNYLTGVI PQELGNMESMI NLDLSQNKLTGS VPDS FGNFTKLESLYLR VNHL
SGA I PPGVANSSHLTTLL LDTNNFTGF FPETVCKGRKLQNI SLDYNHLEGGI PKSLRD
CKSLIRAR FLGAKFTGDI FEAFGI YPDLNF I DESHMKYFIGE I SNEMEKSPKLGALI MS
NNNI TGA I PTEI WMTQLVELDLSTNNLFGELPEA I GNLTNLSRLRLNGNQLSGR VPA
GLS FLYNLESLDLSSNNFSSE I PQTFDS FLKLHDMNLSRLKFDGS I PRLSKLTQLTQL
DLSHNQLDGEI PSQLSSLQSLDKLDLSTNNLFGEL PTTFEGMI ALTNVDI SNNKLEGP
LPDTFTFRATADALEENI GLCSNI FKQRLKPCREJKKPKKNGNLVWNI LVFI LGYLV
ILSI CANTFTYCI RKRKLQNGRNTD PETGENMS I FSVDGKFKYQDI I ESTRNETEPHL
IGTGGYSKVYRANLQDTI I AVKRLHDTI DEEI SKPVYKQEFLNEVKGVAHALSYMHD
RITFI VHRD I SSGNI LLDNDYTAKI SDPGTAKLLKTDSSMSAVAGTYGYVAP BEPAYT
RAMTMET STRUKEGSINI I I E I I TYTHCTIN UTGG I GEG TEGENIE TERMIND
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DEVNMTLAKQEAKLVHEKIKDKHYNDEDVIRILSTRSKAQINATTNRYQDDHGEELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana gb|AF083913. It contains an annexin domain PF [00191. ESTs gb|H76460, gb|Z18518, gb|Z26190, gb|S18518, gb|Z26190, gb|S18518, gb|Z26190, gb|S18518, gb|Z26190, gb|S18518, gb|S2619, gb|S2714, gb|S181940, gb|S1819595, gb|S1819519, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID
LKVIGEVQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"
complement (7937...1730)
/gene="F14D7.3"...
                                                                ANYVIQTALSVTKGPVRAKLVAKVYRYGKLHSSPYCKKIFSKTILKK"
12116. .14526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains PF 00806."
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gb AL161513.
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/gene="F14D7.2"
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join(5917. .599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKVTEKCDVYSFGVLILELIIGKHPGDLVSSLSSSPGEALSLRSISDERVLEPRGQNR
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TNSSKLSSWYHDANTNTSFSCTSWYGVSCNSRGSIEELNLTNTGIEGTFQDFPFISLS
NLAYVDLSMNLLSGTIPPQFGNLSKLIYFDLSTNHLTGEISPSLGNLKNLTVLYLHQN
/note="Contains similarity to Tal-1_transposon gb|X13291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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/db_xref="GI:8778968"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Contains similarity to a putative protein CAB78009
gi|7267527 from Arabidopsis thaliana BAC T32A17
gb|AL161513. It contains Pumilio-family RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Identical to annexin (AnnAt1) mRNA from Arabidopsis
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RNFSSVRVQNNNFHGVSPSPGLLGLQDSFNPNGFEEMMAFKDHKDFLLDHINEPIKRS
PFLRGNDAFKGSLMFEGIRVSQILAAMEGGGASYPDEPKINGGLPLDLVGMVEIYGSV
NLMARDQIGCRALQKLVEEGTVLDSKVIFLEIIDHVVELSMDPLGNYIVQKLLVVSDE
EQRTMIVSVLTSKFRELIKICLNTNGTRVIQKHKTVKTKQQILAVKSALEPGFUTLV
NDSNGYHVLQSCLEFLFVDNNKLRITKLSHILISFLLFUTVKSQDECCEIUQGFVVEN
NDSNGYHVLQSCLEFLFVDNNKLRITKLSHILISFLLFUTVSSDECCEIUQGFVEN
NDSNGYHVLQSCLEFLATQKFSSHVIEKCLKKYPESRAEIVRELLSYPNFEQLL
DQQVSSVNLLLPFRTHGIELATQKFSSHVIEKCLKKYPESRAEIVRELLSYPNFEQLL
                                                                                                /tranelation="msbiygvaryhlytlvyllavysllcikekptrlktlvsbkina kgakifensrlktensbkina kgakifensrlktensbkina kgakifensrlktensbking kgakifensrlktensbking koldyfleteis by the project of the proj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F1407.6"
/gene="F1407.6"
.45134,
join(44612. 44780,45014. 45403,45501. .45644,45676. .46134,
46297. .46476,46633. .47029,47113. .47505,47737. .48082,
48145. .48411,48465. .48541,48632. .48698)
/gene="F1407.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F14D7.5"
/gene="Contains similarity to a putative RNA-binding /note="Contains similarity to a putative RNA-binding protein AAP18550 gi|6587864 from Arabidopsis thaliana T11111 gb|AC012680. It contains Pumilio-family RNA binding domains PF|00806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34873. .35035,35279. .36183))
/gene="F14D7.5"
/note-"677.5"
GPRANELRRMLRQDYALIQPYFKCLLETNPNSLVAMETEKDNSGVERFKYLFFALDAC
VQGYAYMRKVIVIDGTHLRGRYGGCLVAASAQDANFQVFPIAFGIVNSKNDEAWTWFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gi |4063759 tr
gb |AC005561."
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GLSSHPTISNIAANLFCEEGLIGCSSTSTSFKLSLLKHKAFTLEKVDADDEKHKKNED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/protein_id="AAF79886.1"
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/protein_id="AAF79885.1"
/db_xref="GI:8778970"
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/db_xref="GI:8778969"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Strong similarity to a mutator-like transposase
yi|4063759 from Arabidopsis thaliana BAC T14A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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 TTTCGCAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCACAGAAGTGC
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Sequence 240
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 GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
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Inze,D., de Veylder,L. and Vlieghe,K. Identification of novel e2f target genes and Patent: WO 2004035798-A 2461 29-APR-2004; CropDesign N.V. (BS)
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                               GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAAATCAAG
                                                                                                          ACTACCGGTGACTTCAGAAAGCTTTTGGTTTCTCTTTGTTACCTCATACAGGTACGAAGGA
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  GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
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Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
                                                                                                                                                                                                                                                                                            Submitted (28-DEC-2000) Plant Gene Street, Albany, CA 94710, USA 3 (bases 1 to 954)
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AF332435.1 GI:12083277
FLI CDNA.
Arabidopsis thaliana (thale cress)
                                                                                                                                     Submitted (07-MAY-2003) Plant
Street, Albany, CA 94710, USA
Annotation based on July 2002
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana clone C00123

membrane-binding protein annexin (
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                /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                              ocation/Qualifiers
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GAGGAAGGAGATGATGATGACAAGTTCCTTGCACTTTTGAGGGTCAACCATTCAGTGCTTG
                                                                                  ATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAGTCTT
                                                                                                                                                              GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
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                                                             ATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAGTCTT
                                                                                                                                          GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
                                                                                                                                                                                                                        GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
                                                                                                                                                                                                                                               GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
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/note="This clone is now in pUNI 51 vector. Previousl it was in pUNI-T3-D/V5-His-TOPO under the clone number C00123."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAE
GRKVIRQAYHETYGEDLLKTLDKELSNDFERAILLWTLEPGERDALLAMEATKKWTSS
NQVLMEVACTRTSTQLLHARQAYHARYKKSLEEDVAHTTGDFRKLLVSLVTSKYXEG
DEVNWTLAKQBAKLVHEKIKDKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILK
SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID
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/db_xref="GI:12083278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
/product="putative Ca2+-dependent
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Brassica juncea
Brassica juncea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Brassica
AY356355
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Submitted (30-UUL-2003) Department of Plant Sciences, School o Life Sciences, University of Hyderabad, Gachibowli, Hyderabad, Andhra Pradesh 500046, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished 2 (bases 1
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                                                   AGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCAC
                                                                                                                        ATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCAATTG
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                                  AAAAGCGCATTTGATGGATGGGGTACCAACGAGGAATTGATCATATCAATCTTGGCTCAC
                                                                                                    ATGGCGACTCTTAAGGTTTCTTCTTCTGTTCCTTCTCCCTCTGAAGATGCTGAGCAATTG
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SLEEGDEDDKFLGLLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVATRAEID
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Gossypium hirsutum
Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 1141)
Shin,H. and Brown,R.M.Jr.
Direct Submission
Submitted (13-FEB-1977) Botany, The Univ. of Texas at Austin,
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Gossypium hirsutum fiber
U89609
Austin,
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 GAAATGACATAAACAAGGACTT--
                         GCGAGGAAATTCTCAAGAGTCTTGAGGAAGGAGGATGATGACAAGTTCCTTGCACTTT
                                                                                                                                    AGCTGGTCCATGAGAAAATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCT
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/translation="MATLTVPTTVPSVSEDCEQLRKAFSGWGTNEGLIIDILGHRNAE
/kranslation="MATLTVPTTVPSVSEDCEQLRKAFSGWGTNEGLIIDILGHRNAE
QRIMITAKTYAETYGEDLLKALDKELSNDFERLVLLWALDPAERDALLANEATKRWTSS
QRULMEIACTRSANQLLHARQAYHARYKSLEEDVAHTTGDFEKTLLLPLVSSYRYEG
EEVNMMIAKTEAKLJEKSLSDKAYSDDVIRVLATRSKQINATLNHYKUREYGNDINK
DLKADPKDEFLALLRSTVKCLVYPEKYEKVLRLAINRRGTDEGALTRVVCTRAEVDL
KIIADEYQRRNSVPLTRAIVKDTHGDYEKLLLVLAGHVEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3635"
34. .984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="Texas Marker1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Gossypium hirsutum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 497.8;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
GAAGGCTGATCCTAAGGATGAGTTCCTTGCACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; DB 8;
3.8e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dependent membrane binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                      CTACAAAAATGAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
VERSION
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2 (bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium hirsutum (upland cotton)
Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 948)
Delmer, D.P. and Pot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium hirsutum annexin (AnnGh1)
U73746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delmer,D.P. and Potikha,T.S. Structures and functions of annexins Cell. Mol. Life Sci. 53 (6), 546-553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U73746.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACATGTGGAGAATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGAAGATGATGCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGTGCCATTGTCAAGGACACTCATGGAGACTATGAAAAATTGCTGCTGGTACTTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAAGCTATTACCAAAGACACTCGTGGAGAGTTACGAGAAGATGCTCGTCGCACTTCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAGGTCCACAGTGAAGTGCTTGGTCTATCCGGAAAAGTATTTTGAGAAGGTTCTTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGGTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTTCTTCGTT
                        /codon_start=1
/product="anmexin"
/protein_id="AAB87993.2"
/brotein_id="AAB87993.2"
/db_xref="GI:15214410"
/translation="ATLTVPTTVPSVSEDCEQLRKAFSGWGTNEGLIIDILGHRNAEQ
RNLIRKTYAETYGEDLLKALDKELSNDFERLVLLWALDPAERDALLANEATKRWTSSN
RNLIRKTYAETYGEDLLKALDKELSNDFERLVLLWALDPAERDALLANEATKRWTSSN
CYLMEIACTRSANOLLHARQAYHARYKKSLEEDVAHTTGDFHKLLLDLVSSYBYEGE
                                                                                                                                                                                                                                                                                                       /gene="AnnGh1"
/function="worldence suggests that annexins may bind to influence activity of callose synthase"
/note="contains 4 repeats characteristic of other annexins; shows evidence of conserved calcium-binding domains; by comparison with other plant annexins as we as with the size of native cotton fiber annexin, this clone probably lacks 5'coding sequence for only the neterical met; calcium binding protein"
EVNMTLAKTEAKLLHEKISNKAYSDDDVIRVLATRSKAQINATLNHYKNEYGNDINKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="AnnGh1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="21
<1. .948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Gossypium hirsutum"
|mol_type="mRNA"
|strain="Acala SJ-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:15214409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="cotton fibers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:3635"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      post-anthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replaced
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ORIGIN

Query Match Best Local S Matches 669

Similarity

39.7%;

Score 488.6; DB 8; Pred. No. 8.3e-113; D; Mismatches 279;

37

277 181

121 217

157 61 97

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AGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGGAACTGAT
                                                                                                                     GGAGATTACGAGAAGATGCTCGTCGCACTTCTCGGTGAAGATGATGCTTAA
                                                                                                                                                                                                                                                                                                                                                                                 GAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGGAGATGATGACGAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTGCTTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCAATTGAGA
                                                                      GGAGACTATGAAAAATTGCTGCTGGTACTTGCAGGACATGTGGAGAATTGA
                                                                                                                                                                                                  GATGAGTATCAGCGAAGGAACAGTGTCCCACTGACTCGTGCCATTGTCAAGGACACTCAT
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1 (bases 1 to 1112)

Vazquez-Tello,A. and Uozumi,T.

Cloning and characterization of a Lavatera thuringiaca cDNA

Cloning and characterization is stimulated by low
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Breton, G., Vazquez-Tello, A.,
Two novel intrinsic annexins
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BD236006.1 GI:33045776
JP 2002527056-A/28.
1 (bases 1 to 2588)
Blokaberg, L.N.
Materials and method for modification of plant Patent: JP 2002527056.A 28 27-AUG-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LID, FLET
                                                 Eucalyptus grandis
Eucalyptus grandis
Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Myrtales; Myrtaceae; Eucalyptus.
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Local Similarity
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OS Eucalyptus grandis (flooded gum)
PN JP 2002527056-A/28
PD 27-AUG-2002
PF 08-OCT-1999 JP 2000575985
PR 13-OCT-1998 US 09/170862,11-AUG-1999 US 60/
PR 13-OCT-1998 US 09/170867,11-AUG-1999 US 60/
PR 13-OCT-1998 US 09/170867,11-AUG-1999 US 60/
PR 08-OCT-1998 US 09/170867,11-AUG-1999 US 60/
PC 00
CC Materials and method for modification of plant ce
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	COMMENT
Bloksberg, L.N. Materials and n Patent: JP 2002 GENESIS RESEARC	AUTHORS TITLE JOURNAL
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 1293)	REFERENCE
BD236034 GI BD236034.1 GI BD236034.1 GI JP 2002527056-/ Pinus radiata	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
4	RESULT 15 BD236034 LOCUS DEFINITION
2343 TACAAGTACTC 2353	ф
990 AATCAATCCTC 1000	γ
930 CACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTCGGTGAAGATGATGCTTAATC 989	B Q
870 CATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCCTATTACCAAAGA 929	B 8
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750 CTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGG 809	g Q

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ALIGNMENTS

ARC34418

AAC34418 standard; DNA; 1192 BP.

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DT 17-OCT-2000 (first entry)

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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 6580.

XX Hybridisation assay; genetic mapping; gene expression control; which is protein identification; signal transduction pathway; metabolic pathway;

XX protein identification; signal transduction pathway;

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Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; r promoter; termination sequence; ss. control; pathway;

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T-199	T-19	r-19	I-19	T-19	r-19	r-19	I-19	T-19	T-19	T-19	T-19	T-19	T-19	I-19	T-19	P-19	1 1 9	P-19	P-19	110	P-19	P-19	P-19	P-19	3-19	3-19	3-19	3-19 9-19	3-19	3-19	3-19 3-19	3-19	3-19	בינו ערינו ערינו	3-19	3-19	3-19	3-19	3-19	7 1 2	3-19	3-19	13 61	3-19	3-1 1-1	3-19	3-19	3-19	# 19 61-19	L-19	L-199 L-199	
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Best Local Similarity 98.1%;
Matches 1171; Conservative
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                             CAAAACTGGAACTGATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGA
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                                                        CATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAA
                                                                 CATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAA
                                                                                      AATCTTGGCTCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCATGAAAC
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99US-0161406P.
99US-0161359P.
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99US-0161361P.
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99US-0161993P.
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Pred. No. 3.7e-282;
0; Mismatches 17;
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23-APR 1999
24-MAY 1999
05-MAY 1999
06-MAY 1999
07-MAY 1999
11-MAY 1999
                                                                                                                                                                                                                                                                            Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                               Arabidopsis thaliana
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99US-0126785P
99US-01267162P
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99US-0149930 99US-0150864 99US-0151066 99US-0151066 99US-0151066 99US-0151306 99US-01513363 99US-01513758 99US-01513758 99US-01554779 99US-0155659 99US-0155659 99US-0156659 99US-0157865 99US-0157867	908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014 908-014

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            GAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTC
                                          GCTGAGATTGACTTGAAGGTCATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTG
                                                                                                     TTGAGGTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGT
                                                                                                                                                                                               GGCGAGGAATTCTCAAGAGTCTTGAGGAAGGAGATGATGATGACAAGTTCCTTGCACTT
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GAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTC
                                                                                         GGCGAGGAAATTCTCAAGAGTCTTGAGGAAGGAGATGATGATGACAAGTTCCTTGCACTT
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ilarity 98.6%;
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Pred. No. 2.7e-281;
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                                          The invention relates to novel isolated lipid metabolism proteins (LMP) and encoding nucleic acids comprising a polynucleotide sequence encoding a polypeptide that functions as a modulator of seed storage compounds in a plant. The LMP nucleic acid is useful in producing transgenic plants with increased levels of seed storage compound, e.g. lipid, a fatty acid, a starch or a seed storage protein, as markers for specific regions of the genome and for evolutionary and protein structural studies. The present sequence represents an LMP nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                            New lipid metabolism proteins and nucleic acids, useful in producing transgenic plants with increased levels of seed storage compound, e. lipid, a fatty acid, a starch or a seed storage protein.
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                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 73; 115pp; English.
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Query Match
Best Local Similarity 100
Matches 954; Conservative

100.0%; --

Score 954; Pred. No. 229

2e-233 DB 12;

Length

954; 0

Indels

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0

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BP;

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WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                        gene; ss; plant; transgenic; E2Fa/DPa transcription factor;
growth regulator; animal feed product; thale cress;
cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                                                                                                                                                        Inze
                                                                                                                                                                                                               18-OCT-2002; 2002EP-00079408
                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                Thale cress cDNA repressed in E2Fa/Dpa
                                                                                                                                                                                                                           20-OCT-2003; 2003WO-EP011658
                                                                                                                                                                      2004-348466/32.
DB; ADN74567.
                                                                                                                                                                                                    CROPDESIGN
                                                                                                                                                                                        De Veylder L,
                                                                                                                                                                                                                                                                                                expressing plants SeqID
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Altering plant characteristics, useful for producing plants for enzyme opharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or more proteins.

Claim 1; SEQ ID NO 2461; 134pp; English

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up component of the component of

Sequence 954 BP; 288 A; 198 C; 229 G; 239 T; 0 U; 0 Other;

S S 밁 맑 δ 맑 á Query Match Best Local Matches Local Similarity 121 954; 61 94 34 ATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCAATTG CTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCTTGTTGTGG AGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCAC AGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAACCTACGGCGAAGAC AGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCAC ATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCAATTG ilarity 100.0%; Conservative 77.6%; AGGAAAGTCATCAGGCAAGCATACCACGAAACCTACGGCGAAGAC Score 954; DB 12; ; Pred. No. 2e-233; ٥, Mismatches Length 954; Indels <u>,</u> Gaps 153 60 93 273 180 213 120

181

CTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCTTGTTGTGG

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RESULT 6
ABQ66078
ID ABQ66 XX
AC ABQ6
XX
DT 21-A
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Inserting Arab
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EN US20
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                                                                                                                                                        Arabidopsis thaliana; thale cress; plant; transgenic; stress; metabolic pathway; biosynthetic pathway; nutri
             27-JAN-2000;
                                        26-JAN-2001;
                                                                                                                    Arabidopsis
                                                                                                                                             stress; metabolic pathway; b insecticide; antibiotic; ds.
                                                                                                                                                                                                Arabidopsis thaliana polynucleotide SEQ ID NO
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                                        2001US-00770149
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                                                                                                                                                           pathway; nutrition; fungicide;
                                                                                                                                                                       GMO; disease;
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Rameaka
Garcia (
                                                                                                  Claim 1; SEQ ID NO 655; 40pp +
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                                                                                                                                                                                               (KRIC/)
(SLAT/)
(DAVI/)
(ALLE/)
(HOFF/)
                                                                                                                                                                                                                                                                                   (GORL/)
(ANYY/)
(HAMI/)
(PRIC/)
(RAIN/)
                                                                                                                                                                                                                               (HAAS/
(GARC/
                                                                                                                                                                                                                                                         (MATH,
                                                                                                                                                                                                                                             (SEOM)
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                                                                                                                     nucleic acid that hybridizes to Arabidopsis thaliana sequences, fur preparing transgenic plants with increased resistar
                                                                                                                                                               , 19'
19'
19'
                                                                                                                                                      'n.Ĉ
                                                                                                                                                                                      PAGE A.

MATHEW A V.

LEDFORD B L.

WOESSNER J P.

HAAS W D.

GARCIA C A.

KRICKER M.

SLATER T.

DAVIS K R.

ALLEN K.

HOFFMAN N.

HURBAN P.
                                                                                                                                                                                                                                                               PRICE J L.
RAINES T M.
YU Y.
RAMEAKA J G.
PAGE A.
                                                                                                                                                                                                                                                                                               AN Y.
HAMILTON C I
                                                                                                               e.g. for preparing metabolism.
                                                                                                                                                                                                                                                                                                              GORLACH
                                                                                                                                                            An Y, Hami
Page A, M
Kricker M,
                                                                                                                                                             Hamilton CM,
A, Mathew AV,
er M, Slater T,
                                                                                                                                                              Ή
                                                                                                  Sequence Listing;
                                                                                                                                                            Price JL, Raines T
Ledford BL, Woess
, Davis KR, Allen
                                                                                                                                                                           Raines TM,
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                                                                                                  English.
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                                                                                                                                                                     d Y
                                                                                                                                                              Hoffman
                                                                                                                                                                        ×
                                                                                                                       resistance
                                                                                                                                                              Haas WD;
man N;
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The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABQ6542+ABQ6642) or their fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agants (e.g. fungicides, insecticides and antibiotics). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at seqdata.uspto.gov/sequence.html?DocID=999909770149

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Sequence 635 BP; 197 A; 133 C; 147 G; 158 T; 0 U; O Other;

Query Match Best Local S Matches 635 51.6%; Score 635; DB; Pred. No. 5.8 DΒ ٠, م Length 635

635;

Conservative

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Similarity

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GAAACCTACGGCGAAGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAG
                                                                    GAAACCTACGGCGAAGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAG
                                                                                               ATATCAATCTTGGCTCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCAC
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The invention relates to a recombinant polynucleotide comprising any c the 58798 Cotton plant cDNA sequences mentioned in the specification. Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having improved property. Producing a plant having an improved property comprises transforming a plant with a recombinant construct comprising promoter region functional in a plant cell operably joined to a
                                                                                                                                                                                         New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway; drought tolerance; plant disease resistance; galactcomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed o
                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                            Kovalic
                                                                                                                                                                                                                                                                                                                                               (ZHOU/)
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ZHOU Y.
CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance.
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CC with the property, and growing the transformed plant. The polypeptide is CC useful for improving plant cold tolerance, manipulating growth rate in CC plant cells by modification of the cell cycle pathway, improving plant CC plant cells by modification of the cell cycle pathway, improving plant CC plant tolerance, providing increased resistance to plant disease, CC producing galactomannan (or lignin or plant growth regulators), improving plant theat tolerance, improving plant tolerance to berbicides, increasing CC the rate of homologous recombination in plants, improving plant tolerance to extreme osmotic conditions or to pathogens or pests, improving yield by modification of photosynthesis, modifying seed oil or protein yield CC and/or content, improving yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, or improving yield by providing improved CC plant growth and development under at least one stress condition. The CC polynucleotide and polypeptide may also be used in recombinant DNA CC or in computer-based storage and analysis systems. The present sequence is a Cotton plant cDNA of the invention. NOTE: The sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from USFO at CC golynucleotide sequences were available, the remaining 52213 CC polynucleotides and all 58798 protein sequences were not present.
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The invention describes an isolated polynucleotide (I) comprising a nucleotide sequence that is one of 145 fully defined sequences of 221-3415 base pairs (bp), given in the specification, and/or its complements, reverse sequences, or sequences having 75, 90 or 95 % sequence identity to or that hybridise under stringent hybridisation conditions to one of the 145 sequences. The methods and compositions of
                                                                                                                                                                                                                                                                                                                                                                                                                                        programmed cell death; plant development; plant cell cycle; ATL2; bnase; lls; lsdl; nucellin-like aspartic protease; annexin; prohib fen-like protein; rac2; retinoblastoma-related protein; SIWA; TPRI TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like prot gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1; defender against cell death; lethal leaf spot; lesion stimulating seven in absentinia; transcription initiation factor;
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plant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are protein encoded by some of the polynucleotide sequence given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.
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The invention describes a nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to any one of 999 fully defined Arabidopsis thaliana sequences (I) as given in specification e.g., 360, CC 1137, 455, 219, 472 nucleotides, etc, or its fragment (I) is useful as a lowering to the complementary molecules in a cDNA library. (I) is also useful for generating genetically modified and transgenic organisms, cc usually plant cells and plants. A proteen encoded by (I) is useful in screening assays to determine the effect of candidate inhibitors, activators or modifiers of the gene product. The protein is also useful for screening biologically active agents e.g., fungicides and conscitudes. A genetically modified cell, comprising an exogenous nucleic acid, where the nucleic acid comprises transcription regulatory sequences operably linked to a sequence capable of hybridising under stringent conditions to (1) is useful in the study of genetic function and regulation, for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene product. This sequence represents an Arabidopsis thaliana
                     Query Match
Best Local
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Rameaka JG,
Parcia CA,
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                                                                                 Sequence
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LEDFORD B L.
WORSSNER J P.
WORSSNER J P.
GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
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RAINES T M.
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Kricker M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44pp; English.
                                                                                   C; 88 G;
Score 470; DB 10;
Pred. No. 7.8e-110;
0; Mismatches 0;
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Ledford BL, Woessner
, Davis KR, Allen K,
                                                                               167 T; 0
                                                                                 U; 0 Other;
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                                      Length 487;
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CAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGGAACTGATGAAG

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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing a

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RESULT 11
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                                                                                                                                                                                                                                           Eucalyptus oplant cell
                                                                             WPI; 200
P-PSDB;
                                           New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.
                               Claim
                                                                                                     Bloksberg LN,
                                                                                                                                            13-OCT-1998;
11-AUG-1999;
                                                                                                                                                                                                                                                                                    31-OCT-2000
                                                                                                                                                                                                                                                                                                                   AAA67128
                                                                                                                                                                    08-OCT-1999;
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                                                                                                                                                                                                                    Pinus radiata.
                                                                                                                                                                                                                                  transgenic plant;
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                              1; Page 93;
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                                                                                                                    GENESIS F
FLETCHER
                                                                                                                                                                                                                                                                                                                   standard; DNA; 1293
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99US-0148426P
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CATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGA
                                                                                                                                                                          CTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to coding sequences (see AAF44740-F44840 and AR744843-F44844) and proteins (see AAF5714-B55714) involved in programmed cell death (PCD; apoptosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel defender against cell death programmed cell death pathway and forestry plant.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1293 BP; 359 A; 290 C; 313 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 54-55; 142pp; English
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                                                        GCTCCGGACAGCCTTCGCAGGATGGGGAACAAATGAGAAGCTGATCATATCCATATTGGG
                                                                                                           ATTGAGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGC
                                                                                                                                                                AACAATGTCGACTCTCACCGTCCCGCAGCCACTGCCCCCTGTAGCCGATGACTGCGAGCA
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Pred. No. 2.5e-109;
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programmed cell death; plant development; plant cell cycle; ATL2; DAD1; Dnase; lls; lsd1; nucellin-like aspartic protease; annexin; prohibitin; fen-like protein; rac2; retinoblastoma-related protein; SINA; TFIID;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes an isolated polynucleotide (I) comprising a nucleotide sequence that is one of 145 fully defined sequences of 221-3415 base pairs (bp), given in the specification, and/or its complements, reverse sequences, or sequences having 75, 90 or 95 % sequence identity to or that hybridise under stringent hybridisation conditions to one of the 145 sequences. The methods and compositions of the present invention to do with (I) sequences of plant cells, and altering plant development. This sequence encodes a protein associated with the programmed cell death pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1; defender against cell death; lethal leaf spot; lesion stimulat seven in absentinia; transcription initiation factor; testis enhanced gene transcript; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide useful for modulating programmed cell altering the development cycle of plant cells, and subsequently may plant development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1293 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 28-29;
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                                      TCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGGACGTTGCTCA
                                                                                                            GACTTCAAGCAACCAAGTTCTTATGGAAGTTGCTTGCACAAGGACATCAACGCAGCTGCT
                                                                                                                                                      TTGGTCACTTGATCCGGCTGAACGTGATGCGTACTTGGCGAATGAAGCGACGAAAAGATG
                                                                                                                                                                                                                            GGACCTCCTCAAGGCATTGGACAGAGAACTTACCAATGATTTCGAGAGGCTGGTGGTCCT
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Best Local Similarity 67.3%;
Matches 645; Conservative
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RESULT 15

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     CACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTCGGTGAAGATGATGCTTAA
                  CTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAACTGG
                                                                             TCTTGAGGAGGAGATGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTG
                                                                                                  ACAGCTCGGTGCAACACTCAACCACTACAACGAGTATGGAAACGCCATTAACAAGAA
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                                                                                                                     CCACACTACCGGTGACTTCAGAAAGCTTTTGGTTTCTCTTGTTACCTCATACAGGTACGA
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nilarity 67.2%;
Conservative
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99US-0161992P.
99US-0161993P.
99US-0162142P.
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Pred. No. 5.1e-106;
0; Mismatches 314;
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99US-0146388P 99US-014703RP 99US-014703RP 99US-0147704P 99US-0147704P 99US-0147704P 99US-01477192P 99US-0147416P 99US-0148341P 99US-0148341P 99US-014834P 99US-0149728P 99US-0149728P 99US-0149728P 99US-0149728P 99US-0149728P 99US-0149728P 99US-015066P 99US-0151066P 99US-0151066P 99US-0151066P 99US-0151068P 99US-0151303P 99US-015330P 99US-015330P 99US-015368P 99US-0159238P 99US-0159238P 99US-015933PP 99US-015933PP 99US-015933PP 99US-015933PP 99US-015933PP 99US-015933PP 99US-015933PP 99US-015933PP 99US-015933PP 99US-0160815P 99US-0160814P 99US-0161405P 99US-0161405P 99US-0161405P 99US-0161405P 99US-016135PP 99US-016135PP

Search completed: August 22, 2005, 07:26:19 Job time : 813 secs

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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/plasmid="pCMVSPORT_6"

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                                                    /clone="GSLTPGH56ZG07"
/tissue_type="Hormone Treated
                                                                                                                            /organism="Arabidopsis
/mol_type="mRNA"
/strain="Col-0"
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TGTTATCTCTTATCTCCCCTCTCTCTCT-CTTTGATGAGTTTCAAATCGTTTGATTTTGTT
                                                                      GAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTCGG
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                        TGAAGATGATGCTTAATCAATCAATCCTCCACAGAGAAACATAAGCTGCTCTACAGCTTC
                                    TGAAGATGATGCTTAATCAATCAATCCTCCACAGAGAAACATAAGCTGCTCTACAGCTTC
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Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.

KRGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1137)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX815936.1 GI:42472184
HTC; GSLT CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
    Location/Qualifiers
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AAACACTAAAAGTAGAAGAAAAAATGG---CGACTCTTAAGGTT---TCTGATTCTGTTCCTG
                                                                                 AAACACTAAAAGTAGAAGAAAATAGAAAGACTCTTAAGGATAAAAAAATCTGTTCCTG
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/tissue_type="Hormone';
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                               /gene="At1g35720"
                                                                                                                                                                                                                                                                                                                                                             /strain="Col-0"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis"

mol_type="mRNA"
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97.8%;
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Pred. No. 1.9e-265;
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Annotation

Unpublished (2004)

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out

full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

Tenome released by MIPS (Munich Information center for Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 GAGGAAAGTCATCAGGCAAGCATACCACGAAAACCTACGGCGAAGACCTTCTCAAGACTCT
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1 (bases 1 to 1063)

1 (bases 1 to 1063)

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BX838972
BX838972.1 GI:42533055
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Sequences).
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/ESThttp://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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CCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCACACTACCGGTGACTT
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/mol_type="mRNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
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/clone_Tib="Arabidopsis thaliana
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                                                                                                BX815/37...
HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Vagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; chrabidopsis.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Clepet, C.,
                                                     Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                  Unpublished
2 (bases 1
                                                                                                                                                                                                                                   BX815939
BX815939.1 GI:42472187
                                                                                                                                                                                                                                                               966 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH18ZH06 of Hormone Treated Callus of Strain col-0 of Arabidopsis thaliana (thale cress).
                                             Annotation
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libratries construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
                                                                                                                                                                             /clone="GSLTPGH18ZH06"
/tissue_type="Hormone T
/plasmid="pCMVSPORT_6"
1. 966
                                                                                                                                                   /gene="At1g35720"
                                                                                                                                                                                                                                                                                                          db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                    organism="Arabidopsis"
                                                                                                                                                                                                                                                                                                                                             strain="Col-0"
                                                                                                                                                                                                                                                                                                                                                                       _type="mRNA"
Score 947.6; DB 3;
Pred. No. 1.4e-236;
0; Mismatches 4;
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Schachter V., Weissenbach J., Salanoubat M.

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http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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1 (bases 1 to 1034)

1 (castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                               Submitted (18-NOV-2003) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr)
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                                        http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis
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                      Location/Qualifiers
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Best Local Similarity 98.0%;
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                                                                                     GAGGTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCCTTCGTTC
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/db xref="taxon:3702"
/clone="GSLTLS23ZB01"
/tissue_type="Adult vegetative tissue"
/plasmid="pCMVSPORT_6"
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/mol_type="mRNA"
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Pred. No. 1.9e-230;
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OF REPD/GABL-Primary database: http://gabl.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information." ORIGIN Query Match 72.5%; Score 892.2; DB 7; Length 910; Best Local Similarity 99.0%; Pred. No. 4.3e-222; Matches 897; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	/db xref="taxon:3702" /db xref="taxon:3702" /tissue_type="root" /lab host="E. coli TOP10" /clone_lib="MPIZ-ADIS-066" /note="Vector: pCMVSPORTG; Site 1: Sall; Site 2: Not1; /clone_lib="MPIZ-ADIS-066" /note="Vector: pCMVSPORTG; Site 1: Sall; Site 2: Not1; /clone_lib="MPIZ-ADIS-066" /note="Vector: pCMVSPORTG; Site 1: Sall; Site 2: Not1; /clone_lib="MPIZ-ADIS-066" /note="Vector: pCMVSPORTG; Site 1: Sall; Site 2: Not1; /clone_lib="MPIZ-ADIS-066" /note="Vector: pCMVSPORTG; Site 1: Sall; Site 2: Not1; /clone_lib="MPIZ-ADIS-06" /note="Vector: pCMVSPORTG; Site 1: Sall; Site 2: Not1; /clone_lib="MPIZ-Note: Sequencing sites Sall-Not1, /compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, /cstablishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection, PI: Bernd Weisshaar Sequence submission managed by property states and sequence submission managed in the context of the	ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weisshaa@mpiz-koeln.mpg.de Insert Length: 910 Std Error: 0.00 Plate: 1 row: I column: 21 Seq primer: SP6P;. FEATURES Location/Qualifiers 10-910 /organism="Arabidopsis thaliana" /mol type="mRNA" /ecotype="mRNA"	VERSION CF652924.1 GI:37429878 KEYWORDS EST. SOURCE Arabidopsis thaliana (thale cress) SOURCE Arabidopsis thaliana (thale cress) RABIDINE Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 910) AUTHORS Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weisshaar, B. TITLE Single-nucleotide polymorphisms for mapping in Arabidopsis thaliana JOURNAL Genome Res. 13 (6), 1250-1257 (2003) PUBMED 12799357 COMMENT Contact: Weisshaar B	Db 841 TGAGATTGACTTGAAGGTCATTGGAGAGGAGTACCAGGCAGG
RESULT 8 CNSOAC11 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB69ZF06 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress). ACCESSION BX814350	Db 665 TCTCAAGAGTCTTGAGGAGGAGATGACAAGTTCCTTTGGTTGAGGACAAC 724 Qy 741 CATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGGAACAAC 724 Qy 742 CATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAA 800	Qy 501 CAGGTACGAAGGAGATGAAATTGACATTGACATTGACAAAAGCTAAGCTGATCCA 560	Qy 261 TATCTTGTGTGGACCTCTGAACCCGGTGAGCGTGATGCTTATTGGCTTATTGAACCTAC 320	21 AAGTAGAAGAAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGA

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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full
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HTC; GSLT_cDNA.
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Location/Qualifiers
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                                                                                       GATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAGATCAATGCTACTTTT
                                                                                                                                                           ACATTGGCTAAGCAAGCAGAGCTAAGCTGGTCCATGAGAAAATCAAGGACAAGCACTACAAT
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                      ACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAGGACAAGCACTACAAT
  (bases 1 to 865)
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/tissue_type="Flowers
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/strain="Col-0"
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97.9%;
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Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breec
Carl-von-Linne Weg 10, 50829 Koeln,
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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30-L020580-066-004-L08-SP6P MPIZ-ADIS-066 Arabidopsis thaliana cDNA
clone MPIZp2001L084Q 5-PRIME, mRNA sequence
                                                                                                                                                                                                                                                                                             Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabido
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                               Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 843 Std Error: 0
Plate: 4 row: L column: 08
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Schmid, K.J., Soerensen, T.R., Stracke, R.,
Mitchell-Olds, T. and Weisshaar, B.
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                                                                              primer: SP6P;.
                                                        Location/Qualifiers
/mol_type="mRNA"
                      organism="Arabidopsis
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                      AAGCAAAGCTCAGATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAAT 680
                                                                                                         TGAGAAAATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wassilewskija-0; roots from three weeks old plants grown on MS-plates at 26M-0C with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sall-NotI, primer sites and orientation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="MPIZ-ADIS-066"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: Not1; cDNA library from Arabidopsis thaliana, accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="root"
/lab_host="E. coli TOP10"
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/db_xref="GABI:938637"
/db_xref="taxon:3702"
/clone="MPIZp2001L084Q"
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Pred. No. 2.7e-206;
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1 (bases 1 to 814)
Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somervi and Welinder,K.G.
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Tel: +45 96358467
Fax: +45 98141808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Karen G. Welinder
Institut for bioteknologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
               GCTCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAACCTACGGC
                                                                         CAATTGAGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTG
                                                                                                                                  AGAAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAG
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                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/ecotype="Columbia"
/db xref="taxon:3702"
/dev_stage="plane"
                                                                                                                                                                                                                                                        /dev_stage="plant 3 weeks old, three days post infection" /clone_lib="Infected Arabidopsis Leaf" /note="Organ: Leaf; /vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT selected."
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                                                                                                                                                                           Score 786.2; DB 6;
Pred. No. 2.3e-194;
0; Mismatches 3;
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RESULT 11
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                Contact: Karen G. Welinder
Institut for bioteknologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000
Tel: +45 96358467
Fax: +45 98141808
                                                                                                                                                   Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Snermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Snermatophyta; Magnoliophyta; Snermatophyta; Arabidopsis.
                                                                                                                                                                                                                            BU639010
782 bp mRNA linear EST 23-5003A04 Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, sequence.
BU639010
                                                                                                                   Spermatophyta; Magnoliophyta; eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; 1 (bases 1 to 782)
Lundsgaard, M., Emmersen, J., Nielsen, K.L., Wilson and Welinder, K.G.
                                                                                                                                                                                                         BU635010.1
EST.
                                                                                   plants
Unpublished (2002)
                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
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                                                                                                          sequencing
          kgw@bio.auc.dk
Location/Qualifiers
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                                                                                                          of Erysiphe
                                         9000 Aalborg,
                                                                                                          cichoracearum
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AGTGCTTGACAAGACCGGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCA
                      AGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCA
                                                                               AGAGTCTTGAGGAAGGATGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTC
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/mol_type="mRNA"

/mol_type="mRNA"

/ecotype="Columbia"

/db xref="taxon:3702"

/db xref="taxon:3702"

/clone_lib="Infected Arabidopsis Leaf"

/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA

library of Arabidopsis and B. cichoracearum infected lea

from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT

selected."
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1 (bases 1 to 775)

Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S. and Welinder,K.G.

EST sequencing of Erysiphe cichoracearum infected Arabidopsis
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Sohngaardsholmsvej 49, 9000
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Institut for bioteknologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
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BST.
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CGTTGCTCACCACACTACCGGTGACTTCAGAAAGCTTTTTGGTTTCTCTTGTTACCTCATA
                                                                                                                                                                                          TATCTTGTTGTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTAC
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                                                                    GCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTTGAAGAGGA
                                                                                                                                        AATCTTGGCTCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAAC
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                                                                                                                                                                      TATCTTGTTGTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTAC
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ilarity 99.5%;
Conservative
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+45 98141808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev stage="Plant 3 weeks old, three days post infection" /clone lib="Infected Arabidopsis Leaf" /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /ecotype="Columbia"
/db_xref="taxon:3702"
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Pred. No. 8e-181;
0; Mismatches
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    Query Match
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Matches 703; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length CDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Functional Genomics Research
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Large scale analysis of Arabidopsis full-length Unpublished (2002) Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; endicotyledons; core endicots;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
Tosids; eurosids [1]; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-298-36-9060
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                                                                                                                                                                                                                                                                                                                            further details
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57.2%; Sillarity 100.0%; Conservative 0;
                                                                                               /clone lib="RAFL5"
/note="Site_1: SstI; Site_2: XhoI; subjected dehydration-treated(1,2,5,10,24 hr)"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                /dev_stage="rosette plants"
/lab_host="SOLR"
                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                             organism="Arabidopsis"
                                                                                                                                                                                                       clone="RAFL05-15-G22"
  Score 703; DB 1; Lo
Pred. No. 1.3e-172;
0; Mismatches 0;
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                                       Length 703
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507 CGAAGGAGATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAA

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TITLE
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VERSION
KEYWORDS
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AV785121/c
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AV785121 RAFL6 A
mRNA sequence.
AV785121
AV785121.1 GI:1
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 Large scale analysis of Arabidopsis full-length Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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 42
TGTGGTCTCTTAAGTTATATATATGAAGAGCATTGGCC
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Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAACTGATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGG
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                                                      CTCTCTCTCTTTGATGAGTTTCAAATCGTTTGATTTTGTTTCTACAAAAACCTTGTTT
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/note="Site_1: SstI; Site_2:
dehydration (1, 2, 5, 10, 24
hr) treatments"
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/clone="RAFL06-11-P04"
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/db_xref="taxon:3702"
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0; Mismatches 0;
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9	Оу 6 В 1	Qy 6	Qy 5	Qy 5	Query Match Best Local Matches 67	ORIGIN	FEATURES Bource		JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 15 BX836971 LOCUS DEFINITION
947 GIGCTIGACAAGACCAGAGCTTTACTTIGICGAIGTITCTTCGTTCAGCAATCAACAAAAC 806	687 GAGTCTTGAGGAAGAGATGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCA 746	627 AGCTCAGATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAA 686 	567 AATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAA 626 	07 CGAAGGAGATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAA 566 	ch 54.3%; Score 667.8; DB 5; Length 679; al Similarity 99.0%; Pred. No. 2.1e-163; 672; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	/ regaration Analysis chartain / mol type="makk" / ecotype="col-0" / do xref="taxon:3702" / do xref="taxon:3702" / clone="GSLTIL538ZF07" / tissue_type="Adult vegetative tissue" / clone_Tib="Arabidopsis thaliana Adult vegetative tissue Col-0"	http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. Location/Qualifiers 1679	Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr The sequences are based on single pass reads Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA: Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genences).	Unpublished (2004) Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaeron Cromieux CD 5706 - 51067 EVDV CODO: FRANCE	Temple.G., Caboche,M., Weissenbach,J. and Salanoubat,M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation	Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 679) Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard M. Criand C. Ouetiar F. Scarmelli C. Schachter V.	BX836971 BX836971.1 GI:42531054 EST. Arabidopsis thaliana (thale cress) Arabidopsis thaliana	8X836971 679 bp mRNA linear EST 11-FEB-2004 BX836971 Arabidopsis thaliana Adult vegetative tissue Col-0 Arabidopsis thaliana cDNA clone GSLTL338ZF07 5PRIM. mRNA secuence.

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AGAA		1107	Ş
CCTT	. CCCTCTCTCTCTTTGATGAGTTTCAGATCGTTTGATTTTGTTTCTACAAGGGCCTTGT	541	皮
CCIT		1047	Ş
TTAT	ATCAATCAATCCTCCACAGAGAAACATAAGCTGCTCTACAGCTTCTGTTATCTCTTATCT	481	문
TTAT		987	8
IGCT	. AGACACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTCGGTGAAGATGATGCTTA	421	밁
IGCT		927	8
TACC	GGTCATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAAGCTATTACCAA 420	361	皮
TACC		867	Ş
CTTQ	TGGAACTGATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAA 360	301	문
-CI		807	Ş
CAAA	. GTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAC 300	241	븅

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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Sequence 17, Appl
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Sequence 18, Appl
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Sequence 101, Appl
Sequence 2431, Ap
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390 TCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTC	330 GACTTCAAGCAACCAAGTTCTTATGGAAGT 391 GACTTCAAGCAACCAGGTTCTCATGGAAAT	270 GTGGACTCTTGAACCCGGTGAGCGTGATGG	210 AGACCTTCTCAAGACTCTTGACAAGGAGCT	150 TCACAGAAGTGCTGAACAGAGGAAAGTCA? 	90 ATTGAGAACCGCTTTTGAAGGATGGGGTACGAAC 	30 AAAAATGGCGACTCTTAAGGTTTCTGATTCTGTT	Query Match 38.1%; Score 468.6; Best Local Similarity 68.4%; Pred. No. 1. Matches 664; Conservative 0; Mismatche	UT 1 9-325-932A-17 9-325-932A-17 9-325-932A-17 9-325-932A-17 9-21604 NEARL INFORMATION: PPLICANT: Filmn, Barry PPLICANT: Lasham, Annette ITLE OF INVENTION: Compositions affect ITLE OF INVENTION: death and their use ITLE REFERENCE: 1022 URRENT APPLICATION NUMBER: US/09/325,93 URRENT FILING DATE: 1999-06-04 UNDER OF SEQ ID NOS: 206 OFTWARE: PastSEQ for Windows Version 3 Q ID NO 17 LENGTH: 1293 TYPE: DNA ORGANISM: Pinus radiata	ALIGNMENTS	8 95.2 7.7 1301 4 US-09-0 9 95.2 7.7 1516 4 US-09-9 9 93.6 7.6 1957 4 US-09-9 1 92.2 7.5 1302 4 US-09-9 2 85.8 7.0 1300 4 US-09-9 81.4 6.6 2054 4 US-09-9 5 81.4 6.6 2120 4 US-09-9 6 81.4 6.6 2120 4 US-09-9 81.4 6.6 2120 4 US-09-9 81.4 6.6 2130 4 US-09-9 81.4 6.6 2130 4 US-09-9 81.4 6.6 2130 4 US-09-9 80.8 6.6 2386 4 US-09-9 9 80.8 6.6 2386 4 US-09-9 1 80 6.5 1356 4 US-09-0 2 64.8 5.3 2105 4 US-09-7 5 59.4 4.8 1211 4 US-09-7
	TGCTTGCACAAGGACATCAACGCAGCTGCT 	GIGATGCTITATIGGCTAAIGAAGCTACAAAAAGATG: 	CAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCTTGTT	AAGTCATCAGGCAAGCATACCACGAAACCTACGGCGA	GAGGACTTGATCATATCAATCTTGGC 	CCTGCTCCTTCTGATGATGCTGAGCA 	.6; DB 3; Length 1293; 1.3e-127; ches 304; Indels 3; Gaps	ing programmed cell in the modification of forestry 2A	NTS	23-655-1190 Sequence 1190, Ap 19-172-38 Sequence 38, Appl 49-016-4660 Sequence 2750, Ap 49-016-1750 Sequence 2753, Ap 49-016-1299 Sequence 1199, Ap 49-016-1290 Sequence 1199, Ap 49-016-1197 Sequence 1197, Ap 49-016-1198 Sequence 1198, Ap 49-016-1198 Sequence 1198, App 49-016-4604 Sequence 348, App 49-016-4605 Sequence 4604, Ap 49-016-4605 Sequence 4604, Ap 99-016-4605 Sequence 4604, Ap 99-016-4605 Sequence 260, App 99-451-493 Sequence 269, App 99-451-268 Sequence 269, App 99-451-268 Sequence 268, App 99-451-270 Sequence 270, App
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GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Flinn, Annette
TITLE OF INVENTION: Compositions affecting pro
TITLE OF INVENTION: death and their use in the
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 789
TYPE: DNA
ORGANISM: Pinus radiata
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Best Local :
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                                                                                                                     Local Similarity
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LENGTH: 704
TYPE: DNA
ORGANISM: Pinus r
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                                             Best Loc
Matches
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
                                                                                                                                                                                                                                                                                                                        Sequence 21, Application Patent No. 6451604
                                                                          Query Match
                                                          Local Similarity
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CGTCCGAAACACTAAAAGTAGAAGAAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCC
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for Windows
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                                             0,
                                           Score 208.4; DB 3;
Pred. No. 5.1e-51;
0; Mismatches 226;
                                                                                                                                                                             Version
                                              Indels
                                                                        Length
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develo

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GENERAL INFORMATION:

APPLICANT: Plinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting pro

TITLE OF INVENTION: death and their use in the

FILE REFERENCE: 1022

CURRENT APPLICATION UMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206
                                                                                                                                                                                                                                                                                                                            ; SOPTWARE: FASTSEQ for Wir
; SEQ ID NO 18
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-325-932A-18
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 233; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09325932A Patent No. 6451604
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                                                                                                                                                                                                                                               Score 186.2; DB 3
Pred. No. 1.4e-44;
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the modification of forestry plant
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Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CLOULOT
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

NUMBER: OF SEQ ID NOS: 207012
COCCUMBER: OF SEQ ID NOS: 207012
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Matches
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SEQ ID NO 2081
LENGTH: 1332
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
    474
                                         446
                                                                                                                                                           354 GGAAGTTGCTTGCACAAGGACATCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGC
                                                                                                                                                                                                                                          294 TGATGCTTTATTGGCTAATGAAGCTACAAAAAGATGGACTTCAAGCAACCAAGTTCTTAT
                                                                                                                                                                                                                                                                                       266
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                                                                                                                                                                                                                                                                                                                                                                  206 GCTGATTGTTAAGGAATATCAAGCAGCATATGGAAAGGAGCTGAAAGATGACTTGAAGGG
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  GCTTTTGGTTTCTCTTGTTACCTCATACAGGTACGAAGGAGATGAAGTGAACATGACATT 533
                                                                             TCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCACACTACCGGTGACTTCAGAAA
                                                                                                                         TGAAATCTTAACTACCAGGACAAGCAGGCAAATGAAGGATATCTCTCAAGCCTATTATAC
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Pred. No. 2.1e-33;
0; Mismatches 468;
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RESULT 6
US-09-023-655-1149
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                          FILING DATE: CLASSIFICATION:
                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: PALO ALTO
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Best Local Similarity 49.0
456; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1339 base pair
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IMMEDIATE SOURCE:
LIBRARY: GENBA
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CAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAA
                                    CCGAATAATGGTGTCCAGATCAGAAATTGACCTTTTGGACATTCGAACAGAGTTCAAGAA
                                                                                                              TTTAGCCGAAAGACTGCATCGAGCCTTGAAGGGTATTGGAACTGATGAGTTTACTCTGAA
                                                                                                                                               CTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGGAACTGATGAAGGAGCACTCAC
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Pred. No. 2.1e-33;
0; Mismatches 468;
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; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-722
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 722
LENGTH: 1339
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GENERAL INFORMATION:
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ORGANISM: Human
-09-949-016-722
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                          GGCCAAACAAGATGCCCAGATTCTCTATAAAGCTGGTGAGAACAGATGGGGCACGGATGA
                                                                                                             AGCTCTGTTGACTTTGGCAGATGGCAGAAGAGATGAAAGTCTGAAAGTGGATGAGCATCT
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Pred. No. 2.1e-33;
0; Mismatches 468;
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                      RESULT 9
US-09-023-655-1152
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US-09-325-932A-19
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; SEQ ID NO 19
; LENGTH: 221
; TYPE: DNA
; ORGANISM: Pinus r
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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Composi
TITLE OF INVENTION: death (
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
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                                                                                                                                                                                                                                                                                                                           359 TTGCTTGCACAAGGACATCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTCGCT
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1152, Application US/09023655
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                                                                                                             TEGTACCTCTTGTGAGCTCCTACCGTTATGATGGAGATGA
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Pred. No. 1.1e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PATELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                           Local
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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   AGATCATCTGCTCCAGAACCAACCAGGAGCTGCAGGAAATTAACAGAGTCTACAAGGAAA
                              AAGTTGCTTGCACAAGGACATCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTC
                                                                                             ATGCTTTATTGGCTAATGAAGCTACAAAAAGATGGACTTCAAGCAACCAAGTTCTTATGG
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Pred. No. 5.3e-20)
                                                                                                                                                                                                                                                                                                                                                                            Mismatches 487;
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FILE REFERENCE: 2048-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 101
LENGTH: 1362
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                            US-09-814-915A-101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 101, Application Patent No. 6750015 GENERAL INFORMATION:
                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone
TITLE OF INVENTION: Thereto
                                                                                                          Local Similarity
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  ATACTAACTTTGATGCTGAGCGGGATGCTTTGAACATTGAAACAGCCATCAAGACCAAAG
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Sequence 2431, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
TITLE OF INVENTION: WITH HUMAN DISEASE, ME
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/99/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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US-09-949-016-2431
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 2431
PRIOR THE SEQ IS NOW NUMBER: 6144
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Best Local Similarity
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ORGANISM: Human
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   GCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGA
                                       TCAGAATCATGGTCTCCCGCAGTGAAGTGGACATGTTGAAAATTAGGTCTGAATTCAAGA 1041
                                                                                                             ATTTTGCTGATCGGCTGTATGACTCCATGAAGGGCAAGGGGACGCGAGATAAGGTCCTGA
                                                                                                                                             ACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAACTGGAACTGATGAAGGAGCACTCA
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Pred. No. 5.9e-20;
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GENERAL INFORMATION:
APPLICANT: KASET, MATCHEW R.
APPLICANT: KASET, MATCHEW R.
TITLE OF INVENTION: GENES EXPRESSED IN TREAT
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGRAM
SEQ ID NO 393
LENGTH: 1660
TYPE: DNA
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Patent No. 672706
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Best Local :
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No.
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                                                      CTGATTGACCAAGATGCTCGGGATCTCTATGACGCTGGAGTGAAGAGGAAAGGAACTGAT
                                                                                     TTGGCTAAGCAAGAAGCTAAGCTGGTCCATGA---GAAAATCAAGGACAAGCACTACAAT
                                                                                                                          TGATGGTTGGCCCTGGCAAAGGGTAGAAGAGCAGAGGATGGCTCTGTCATTGATTATGAA
                                                                                                                                                           TTTTGGTTTCTCTTGTTACCTCATACAGG----TACGAAGGAGATGAAGTGAACATGACA
                                                                                                                                                                                                                                                                 AGATCATCTGCTCCAGAACCAACCAGGAGCTGCAGGAAATTAACAGAGTCTACAAGGAAA
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Pred. No. 1.
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APPLICANT: Tait, Jonathan

APPLICANT: Tait, Jonathan

APPLICANT: Brown, David

ITITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITE

FILE REFERENCE: UOFW-1-13841

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.0

SEQ ID NO

LENGTH: 981

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(981)
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                                                    GANACCTACGGCGAAGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAG
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Pred. No. 1.9e-19;
0; Mismatchés 484;
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Sequence 3, Application US/09324096A
Patent NO. 6323313
GENERAL INFORMATION:
APPLICANT: Talt, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENI
FILE REFERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 981
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-324-096A-3
                                                                  Query Match
Best Local S
Matches 418
                                                                                                                                       NAME/KEY: CDS
LOCATION: (1)..(981)
.09-324-096A-3
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                                                              Score 101.6; DB 3;
Pred. No. 1.9e-19;
0; Mismatches 484;
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GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
                                                                                                                    Sequence 5, Application US/09324096A Patent No. 6323313
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CURRENT FILING DATE: 1999-06-01
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                                                        GAGATTGACTTGAAGGTCATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTGGAG
                                                                                                         GCAATCAACAAAACTGGAACTGATGAAGGAGCACTCACTAGAATTTGTGACCACAAGAGCT
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                                                                                       GCTATGAAGGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGT
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Db 913 TCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGA 972

Qy 973 GAAGATGA 980
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Search completed: August 22, 2005, 03:09:22
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Result
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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/ Cgm2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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/ Cgm2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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/ Cgm2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/ Cgm2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
  ) 21 US-10-690-564-1

; 9 US-09-770-119-655

11 9 US-10-767-795-4242

5 18 US-10-425-114-7439

5 18 US-10-425-114-29928

18 US-10-424-599-1190

14 US-10-219-220-218
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Sequence 1, Appli
Sequence 655, App
Sequence 4242, Ap
Sequence 7439, Ap
Sequence 29928, A
Sequence 1190, Ap
Sequence 218, App
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US-10-690-564-1
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CURRENT FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Kopatentin 1.71
SEQ ID NO 1
LENGTH: 1230
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10690564
Publication No. US20050089872A1
GENERAL INFORMATION:
APPLICANT: KOREA KUMHO PETROCHEMICAL CO., LTD
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ANNEXINS FROM PLANTS
FILE REFERENCE:
                                                                                                                                                  Query Match
Best Local Similarity
Matches 1230; Conserv
  61
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GTTCCTGCTCCTTCTGATGATGCTGAGCAATTGAGAACCGCTTTTGAAGGATGGGGTACG
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CATTGGCCTAAAAAAAAAAAAAAAAAAAAA 1230
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APPLICANT: Hoffman, Neil
APPLICANT: Hutban, Patrick
TITLE OF INVENTION: Expressed Sequences of
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (pARA-0.13 prv)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 655
LENGTH: 635
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 655, Application US/09770149
Patent NO. US20020059663A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Yu, Yang
APPLICANT: Raeaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Hedford, Brooke L.
APPLICANT: Hedford, Brooke L.
APPLICANT: Hoessner Jeffrey P.
APPLICANT: Hoessner Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Slader, Ted
APPLICANT: Bavis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
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Best Local Similarity
Matches 635; Conserv
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TCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAA
                                                                                    GANACCTACGGCGAAGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAG
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                                                             51.6%; Score 635; DB 9; Le ilarity 100.0%; Pred. No. 1.6e-169; Conservative 0; Mismatches 0;
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RESULT 3
US-10-767-795-4242
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KOVALIC, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 4242
LENGTH: 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4242, Application US/10767795 Publication No. US20040181830A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Gossypium hirsutum
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                                                                        AAACACTAAAAGTAGAAGAA-AAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTC
                                                                                                                  TTGAGAGGCTGGTTTTGCTTTTGGCTCTTGATCCTGAACGTGATGCCCTTTTTGGCTA
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Pred. No. 2.3e-130;
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7439
LENGTH: 1145
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
FILE REFERENCE: 38-21 (53313) B
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RESULT 5
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  Sequence 29928, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
FULE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 29928
LENGTH: 1145
TYDEP: NUM
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Best Local S
Matches 672
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                                                                     AGGAAATTCTCAAGAGTCTTGAGGAAGGAGATGATGATGACAAGTTCCTTGCACTTTTGA
                                                                                                         CCACAAGGAGCAGAGCACAGATTAATGCTACTTTGAATCACTACAAAGATGCATTTGGAC
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Pred. No. 3.3e-125;
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 1190
LENGTH: 1393
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Best Local
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ORGANISM: Glycine max
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                                           CATCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTG 433
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                   CCTCTGAACAATTGTTTGCTGCGAGGAAGGCTTACCATGTTCTTTATAAGAAGTCTCTGG
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; TYPE: DNA
; ORGANISM: Eucalyptus
US-10-219-220-218
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CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US2003(
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 218
SEQ ID NO 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 218, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                          Matches
                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
                                                                                                                        Local Similarity
nes 664; Conserv
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Pred. No. 1.8e-123;
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Sequence 28, Application US/10393840
Publication No. US20030229922A1
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Cell Wa
FILE REFERENCE: 11000.1012c3
CURRENT APPLICATION NUMBER: US/10/393,840
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PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR PILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/170,862
PRIOR PILING DATE: 1998-10-13
PRIOR PILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 956
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 2588
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; ORGANISM: Eucalyptus
US-10-393-840-28
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Best Local Similarity
Matches 666; Conserv
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                    CCTGACTCGCCCTGAGAAGTATTTTGAAAAGGTTCTTCGTCTAGCCATCAATAAGCGAGG
                                                   CTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGG
                                                                                                          TCTTGAGGAAGGAGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTG
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APPLICANT: Hurban, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 20026 (PARA-015PRV)
CURRENT APPLICATION NUMBER: US/09/770,961
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,466
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 765
LENGTH: 487
TYPE: DNA
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US-09-770-961-765/c
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Best Local Similarity
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
 GAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGG
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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                                                                 AGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAG
                                                                                                       GAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGG
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                                      AGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAG
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Kricker, Maja
Slader, Ted
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Rameaka, Joshua G.
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                                                                                                                                                                                                                                                              38.2%; Score 470; DB 10; 100.0%; Pred. No. 1.1e-122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Plinn, Barry
APPLICANT: Lasham, Annette
ITITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Cleath and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1293
TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 38.1%;
Local Similarity 68.4%;
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TATGGCAAGACAAGCATATCATGCCCGATACAAGAAGTCAATGGAAGAGGACGTCGCTCA
                         TCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCA 449
                                                                     GACTTCAAGCAACCAGGTTCTCATGGAAATAGCCTGCACGAGGTCTCCGCAGCAGTTGCT
                                                                                        GACTTCAAGCAACCAAGTTCTTATGGAAGTTGCTTGCACAAGGACATCAACGCAGCTGCT
                                                                                                                                                               GTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTACAAAAAAGATG
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O; Mismatches 304;
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GENERAL INFORMATION:

APPLICANT: Bloksberg, Leconard N.

APPLICANT: Bloksberg, Leconard N.

ITILE OF INVENTION: Materials and Methods for the

FITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides

FILE REFERENCE: 11000.1012c3

CURRENT APPLICATION NUMBER: US/10/393,840

CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: US 09/636,800

PRIOR APPLICATION NUMBER: US 09/170,862

PRIOR APPLICATION NUMBER: US 09/170,862

PRIOR APPLICATION NUMBER: US 60/148,426

PRIOR APPLICATION NUMBER: US 60/148,426

PRIOR FILING DATE: 1999-00-11

PRIOR APPLICATION NUMBER: PCT NZ/99/00169

PRIOR FILING DATE: 1999-10-08

NUMBER OF SEG ID NOS: 956

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH. 1203
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US-10-393-840-109

Sequence 109, App

Publication No. (

GENERAL INFORMAT:

APPLICANT: Bloke

TITLE OF INVENT:

TITLE OF INVENT:

TITLE REFERENCE:

CURRENT FILING I

PRIOR APPLICANT:

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PRIOR BUILTONTO.
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Best Local Similarity
Matches 664; Conserv
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                                                                                                                                      LENGTH: 1293
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NO 10772
LENGTH: 1145
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
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                                                                  CCACAAGAAGCAAAGCTCAGATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCG
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                                                                                                     TGCTGCATGAGAAGATTTCAAACAAGGCTTATAATGATGACGACTTCATCAGGATTTTGG
                                                                                                                          TGGTCCATGAGAAAATCAAGGACAAGCACTACAATGATGAGGGATGTTATTAGAATCTTGT
                                                                                                                                                       GTTCTTATCGATATGAAGGAGATGAGGTCAACTTGACCCT-GCAAAAACTGAGCAAAAAT
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ACAAGATATCAACAAGGACTGA - AGGCTGATCCAAAGGACGAGTTCCTGTCTTTACTAA
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Pred. No. 6.6e-117;
0; Mismatches 311; ]
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US-10-424-599-70457
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APPLICANT: Kovalic David K
APPLICANT: Shou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 70457
LENGTH: 1321
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_34633C.
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386 TGCTTCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTG
                                                                                                                                                                                                                                                                                                   206 GCGAAGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 GAAGAAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTG
                                                TGTTGACTTCAAACAATTGGGTCATTTTGGAAATTGCTTCCACTAGATCTTCACTTGATC
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Pred. No. 2.7e-111;
0; Mismatches 312;
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; NUMBER OF SEQ ID NOS: 290
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 20
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-219-220-20
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US-10-219-220-20
                                                                 Query Match
Best Local Similarity
Matches 508; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/10219220 Publication No. US20030082724A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                         APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR PILING DATE: 1999-06-04
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PRIOR FILLING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR FILLING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 956
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 26
LENGTH: 789
                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/10393840 Publication No. US20030229922A1 GENERAL INFORMATION:
                                                                                                                                                                                                                APPLICANT: Bloksberg, Leonard N. TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Cell Wall FILE REFERENCE: 11000.1012c3
CURRENT APPLICATION NUMBER: US/10/393,840
CURRENT FILING DATE: 2003-03-20
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Pred. No. 1.2e-139;
Mismatches 0;
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RESULT 3
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 02-AUG-2002; 2002US-0400803P
                                     04-AUG-2003; 2003WO-US024364
                                                                                                                                                                                        plant; lipid metabolism protein; LMP; seed storage compound;
transgenic plant.
                                                                                                               WO2004013304-A2
                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                  Plant
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Local Similarity 100.0%;
hes 317; Conservative 0
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Pred. No. 1.2e-139;
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RESULT 4
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                                                                                                                                                           plant; transgenic; E2Fa/DPa transcription factor; growth regulator animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                     WO2004035798-A2
                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                       Thale cress
                                                                                                                                                                                                                                                                                                                               15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN74567 standard; protein; 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       he invention relates to novel isolated lipid metabolism proteins (IMP) nd encoding nucleic acids comprising a polynucleotide sequence encoding polypeptide that functions as a modulator of seed storage compounds in plant. The LMP nucleic acid is useful in producing transgenic plants with increased levels of seed storage compound, e.g. lipid, a fatty acid, starch or a seed storage protein, as markers for specific regions of the genome and for evolutionary and protein structural studies. The resent sequence represents an LMP of the invention.
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Pred. No. 1.2e-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC This invention relates to a novel method for altering one or more plant CC characteristics. Specifically, it refers to identifying genes that are up CC - or down-regulated in transgenic plants overexpressing the heterodimeric CC E2Fa/DFa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes CC generating transgenic plants for the production of growth regulators, CC enzymes, therapeutics, pharmaceuticals and animal feed products, where CC the altered plant characteristics are selected from increased yield or the altered plant characteristics are selected from increased yield or CC transduction, storage lipid mobilisation, biochemistry, signal CC transduction, storage lipid mobilisation and/or altered photosynthesis, CC each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers CC during transformation of cells or tissues. The identified genes play a crole in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale crees protein capressed by a gene repressed 1.3 fold or more in plants overexpressing CC thrention.
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Matches 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2462; 134pp; English.
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                 RGDYEKMLVALLGEDDA 317
                                                                                               TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                                                                        DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
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                                                                     TRPELYFVDVLRSAINKTGTDEGALTRIVTTRABIDLKVIGEEYORRNSIPLEKAITKDT
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99US-01211825p 99US-0122180p 99US-0122788p 99US-0122782p 99US-0123782p 99US-	(first entry) (first entry) thaliana protein fragment SEQ ID NO: 7038. trification; signal transduction pathway; metabolic pathway; sequence. sequence.
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           Score 1611; DB 3;
Pred. No. 1.3e-139;
Mismatches 0;
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RESULT 7
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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polypeaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are
                                                                                                                                                                                                                                                                                                                                                                                        New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.
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                                                            New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.
                    Claim 17;
                                                                                                                                                    WPI; 2000-339328/29.
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RESULT 9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
 WPI; 2001-061724/07
                                  Flinn
                                                                                                                   04-JUN-1999;
                                                                                                                                                02-JUN-2000; 2000WO-NZ000086
                                                                                                                                                                                  14-DEC-2000!
                                                                                                                                                                                                                   WO200075331-A1
                                                                                                                                                                                                                                                                                                  Cell death modulator; programmed cell death; PCD; apoptosis;
                                                                                                                                                                                                                                                                                                                                 Annexin-like protein
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les 226; Conserv
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                                                                 GENESIS R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKAYGHEDLIRILATRSKAQVNATLNHYKNEFGNDINKDLKT-DPKDAFLTILRATVKCL
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                                                                                                               99US-00325932
                                                                 RES & DEV CORP LTD.
R CHALLENGE FORESTS LTD
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ADB94698
ADB94698
ADB94698
AC ADB94
XX ADB94
XX DAB94
XX DAB94
XX DAB96
XX DAB96
XX DAB96
XX Progr
KW Dnase
KW Fen-1
KW TEGT-1

Pinus radiata. US2003082724-A1

enhanced

gene transcript.

programmed cell death; plant development; plant cell cycle; ATL2; DAD1; Dnase; lls; lsdl; nucellin-like aspartic protease; annexin; prohibitin; fen-like protein; rac2; retinoblastoma related protein; SIMA; TFIID; TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like protein; gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1; defender against cell death; lethal leaf spot; lesion stimulating death; seven in absentinia; transcription initiation factor;

Programmed cell death pathway protein annexin

#1.

04-DEC-2003

(first entry)

ADB94698 standard;

protein;

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Matches 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 70-71; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel defender against cell death programmed cell death pathway and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF44756.
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Similarity 71.3%;
26; Conservative 3
            RGDYEKMLVALLGEDDA 317
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                                                            TRPEKY FEKVLRLAINKRGTDEGALTR VVATRAEVDMKFISEEY QRRNSIPLDRAIVKDT
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 TGDYEKMLLALIGHVEA
                                                                                                                                EKAYGHEDLIRILATRSKAQVNATLNHYKNEFGNDINKDLKT-DPKDAFLTILRATVKCL
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316
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Pred. No. 3.8e.
99; Mismatches
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RESULT 11
ADB94896
ID ADB94
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AC ADB94
XX
AC ADB94
XX
DT 04-DE
DT 04-DE
CX
DE Progr
XX
CW Drogr
KW Drogr
KW Drase
KW TEGT;
KW Gp 91
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Best Local
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programmed cell death; plant development; plant cell cycle; ATL2; DAD1; DRASE; l1s; lsd1; nucellin-like aspartic protease; annexin; prohibitin; fen-like protein; rac2; retinoblastoma-related protein; SINA; TFIID; TEGT; xylogenic Rnase; pur-alpha; cyreine protease; RPP5-like protein; gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1;
                                                                                                                        04-DEC-2003
                                                                                                                                                                                 ADB94896
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                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                     RGDYEKMLVALLGEDDA
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                                                                                        death pathway protein annexin
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71.3%;
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; Pred. No. 3.8e-99;
39; Mismatches 51
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plant cells, and subsequently modifying
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RESULT 12 AAG09201 ID AAG09 XX

AAG09201

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Best Local Similarity
Matches 218; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide useful for modulating programmed cell death, altering the development cycle of plant cells, and subsequently modifyin plant development.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 316
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Search completed: August 19, 2005, 20:40:41 Job time : 169 secs

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ALIGNMENTS

probable annexin protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: C86479

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

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A;Molecule type: DNA
A;Residues: 1-317 <STO
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Matches 317; Conserv
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                                                                                                                                                                                                                                                                                                                                              MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
                                                                                                                                                                                                                                                                                                                                                                  MATLKVSDSVFAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
                                                        TRPELYFYDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYORRNSIPLEKAITKDT
                                                                                                                           DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1611; DB 2;
100.0%; Pred. No. 1.6e-97;
tive 0; Mismatches 0;
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Indels

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Gaps

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60

62

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fiber annexin - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31428
R;Shin, H; Brown, R.M.
submitted to the EMBL Data Library, February 1997
A;Reference number: Z21028
A;Accession: T31428
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRUA
A;Residues: 1-316 <SHI>
A;Cross-references: UNIPROT:082090; EMBL:U89609; NID:g3493171; PID:g3493172
A;Experimental source: strain Texas Marker1
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding
                                                 annexin - upland cotton (fragment)
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #
C;Accession: T10805
R;Potikha, T.S.; Delmer, D.P.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z17161
A;Accession: T10805
A;Reterence number: Z17161
A;Accession: T10805
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T10805
A;Residues: 1-315 <POT>
A;Cross-references: UNIPROT:P93157; EMBL:U73746; NID
A;Experimental source: strain Acala SU-2; cotton fib
C;Genetics:
A;Note: AnnGh1
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding
F;85-156/Domain: annexin repeat homology <AXR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
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73.5%;
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0.0%;
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Pred. No. 5.3e-71;
7; Mismatches 45
Score 1128.5; DB Pred. No. 3.4e-66;
                                                                                                                                                                                                                             from GB/EMBL/DDBJ
                                                                                                                                                   EMBL:U73746; NID:g1843524; PID:g1843525 SJ-2; cotton fiber
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C;Species: Capsicum a
C;Date: 15-Feb-1997 #
C;Accession: S66274
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status preliminary; nucleic acid sequence not shown
A;Status preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-314 <PRO>
A;Cross-references: UNLPROT:Q42657; EMBL:X93308; NID:g1071659; PIDN:CAA63710.1;
A;Note: the sequence of residues 155-230 is shown in line for annexin (alfalfa)
C;Superfamily: annexin ; annexin repeat homology
F;14-85/Domain: annexin repeat homology <AX1>
F;14-85/Domain: annexin repeat homology <AX2>
F;169-238/Domain: annexin repeat homology <AX4>
F;169-238/Domain: annexin repeat homology <AX4>
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                                       TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                 DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEBILKSLEEGDDDDKFLALLRSTIQCL
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                     VYPEHYFVEVLRDAINRRGTEEDHLTRVIATRAEVDLKIIADEYQKRDSIPLGRAIAKDT
                                                                                            ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK
                                                                                                                                                                                                                                                                                                                        MASLTVPAHVPSAAEDCEQLRSAFKGWGTNEKLIISILAHRTAAQRKLIRQTVAETFGED
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                                                                                                                                                                      AREAYHARYKKSLEEDVAYHTTGDHRKLLVPLVSSYRYGGEEVDLRLAKAESKILHEKIS
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Pred. No. 1.7e-65;
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Length

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annexin, isoform P35 - tomato

C;Species: Lycopersicon esculentum (tomato)

C;Species: Lycopersicon esculentum (tomato)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_ch

C;Accession: T06322; S11463; S11462

R;Lim, E.K.; Roberts, M.R.; Bowles, D.J.

J. Biol. Chem. 273, 34920-34925, 1998

A;Title: Biochemical characterization of tomato annexin p35

A;Reference number: Z15591; MUID:99074266; PMID:9857021

A;Accession: T06322

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-315 <LIM>
A;Residues: 1-315 <LIM
A;Residues: 1-315 
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A;Experimental source: strain Acala SJ-2; cotton fiber
C;Genetics:
A;Note: AnnGh2
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding
C;Keywords: calcium binding
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A;Cross-references: UNIPROT:O81535; EMBL:AF079231; A;Experimental source: tissue type root R;Smallwood, M.; Keen, J.N.; Bowles, D.J. Biochem. J. 270, 157-161, 1990
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A; Accession: T10807
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Pred. No. 8.3e-65;
3; Mismatches 53;
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n 16-Jul-1999 #text_change 09-Jul-2004
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                                                                                           NID:g3378203;
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Plant Physiol. 104, 1463-1464, 1994
Plant Physiol. 104, 1463-1464, 1994
A;Title: The cDNA sequence encoding an annexin from Medicago
A;Reference number: Z16735; MUID:94286751; PMID:8016273
                                                                                                                                                                                                                                                                                                                                                                             annexin - alfalfa (fragment)
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
C;Accession: T09552
R;Pirck, M; Hirt, H; Heberle-Bors, E
                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 <PIR>
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A;Residues: 108,'X',110,'X',112-119,'X',121-127,'R',129,'X',131-133,'HI',136-141,'S'
A;Accession: S11462
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                                                                                                                                                                                         A;Gene: ann
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A; Residues: 'EXNI', 175-177,'EX', 180-181,'X', 183-184,'N', 186-192,'L', 194-195,'X', 197,'X'
                                                                                                                           ;Superfamily: annexin I; annexin repeat homology;Keywords: calcium binding; phospholipid binding;7-78/Domain: annexin repeat homology <AXR>
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Pred. No. 3e-62;
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Pred. No. 4.7e-63;
7; Mismatches 59
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RESULT
T02961
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N;Alternate names: protein T31P16.220
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50027
R;Bevan, M; Zimmermann, W; Grueneisen, A.; Wambutt, R.; Kalicki, J.; Wohle submitted to the Protein Sequence Database, May 2000
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A;Introns: 26/1; 74/3; 147/3
C;Superfamily: annexin I; annexin repeat homology
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A;Molecule type: DNA
A;Residues: 1-316 <BEV>
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A, Reference number: Z25027
A, Accession: T50027
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                                                                                                                    TYPEKYFEKVLRQAINKLGTDEWGLTRVVTTRAEFDMERIKEEYIRRNSVPLDRAIAKDT
                                                                                                                                    TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                                                                                                                                          AKQAYQARYKTSLEEDVAYHTSGDIRKLLVPLVSTFRYDGDEVNMTLARSEAKILHEKIK
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                                                                                        RGDYEKMLVALLGEDDA
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Pred. No. 2.7e
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A;Cross-references: UNIPROT:Q9LX08; EMBL:AL356332; GSPDB:GN00063; A;Experimental source: cultivar Columbia; BAC clone T31P16 C;Genetics:
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N;Alternate names: protein T31P16.210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50026
C;Accession: T50026
R;Bevan, M; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Kalicki, J.; Wohle submitted to the Protein Sequence Database, May 2000
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T50026
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(;Species: Zea mays (maize)

(;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_chanc

(;Accession: T02961

R;Battey, N.H.; James, N.C.; Greenland, A.J.

Plant Physiol. 112, 1391-1396, 1996

A;Title: CDNA isolation and gene expression of maize annexins

A;Reference number: Z14796; MUID:97092863; PMID:8938425

A;Accession: T02961
                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-318 <BEV>
A; Cross-references: UNI
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A; Accession: T50026
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A; Residues: 1-314 < BAT>
                                                                                                  A; Map position: 5
A; Introns: 26/1; 74/3; 147/3
                                                                                                                                          C;Genetics:
A;Gene: ATSP:T31P16.210
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                  Query Match
Best Local (
Matches
                                                                               Superfamily:
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Best Local :
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                                                                                 annexin I; annexin repeat homology
  Conservative
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  52;
Score 991.5; 1
Pred. No. 2.6e
52; Mismatches
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                  DB 2;
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annexin P35 - maize

C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 0:
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 0:
C;Accession: T02975
R;Battey, N.H.; James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A;Title: CDNA isolation and gene expression of maize annexins P33
A;Reference number: Z14796; MUID:97092863; PMID:8938425
A;Accession: T02975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNIPROT:043864; EMBL:X98245; NID:91370602; PII
A;Cross-references: UNIPROT:043864; EMBL:X98245; NID:91370602; PII
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
;Accession: T02975
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                                                                                                             DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
                                                                                                                                                                                                                                          ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
                                                              RGDYEKMLVALLGED 315
                                                                                                                                                         KKAYSDEEIIRILTTRSKAQLLATFNSYKDQFTHAINKDL-KADPKDEFLSTLRAIIRCF
                                                                                                                                                                                                                        VKQAYHDRFKRSLEEDVAAHVTGDFRKLLVPLVSAYRYDGPEVNTSLAHSEAKILHEKIH 180
                                                                                                                                                                                                                                                                                    LLRALGDEIHGKFERAVILWTLDPAERDAVLANEEAKKSHPGGRALVEIACARTPAQLFA
                                                                                                                                                                                                                                                                                                                                                 MATLTVPSSVPAVAEDCEOLHKAFEGWGTNEKLIISILAHRNAAOARAIRRGYAEAYGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTRGDYEKMLVALLGEDDA 317
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                                                                                           TCPDRYFEKVIRLALGGMGTDEDDLTRVVTTRAEVDLKLIKEAYQKRNSVPLERAVAKDT
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                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 949.5; DB 2
Pred. No. 1.4e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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MATIRVPNEVPSPAQDSETLKQAIRGWGTDEKAIIRVLGQRDQSQRRKIRESFREIYGKD
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RESULT

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probable annexin [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) (195ecies: Arabidopsis thaliana (Mouse-ear cress) (196ecies: Arabidopsis thaliana (196ecies: Ara
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R;Wilkinson, J.Q.; Lanahan, M.B.; Conner, T.W.; Klee, H.J.

Plant Mol. Biol. 27, 1097-1108, 1995

A;Title: Identification of mRNAs with enhanced expression

A;Reference number: S56673; MUID:95284359; PMID:7766892
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C;Species: Fragaria x ananassa (garden strawberry)
C;Date: 10-Oct-1995 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-321 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: A84809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Sequence and analysis of chromosome A; Reference number: A84420; MUID: 20083487; PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: annexin I; annexin repeat homology F;42-113/Domain: annexin repeat homology <AX2>F;125-196/Domain: annexin repeat homology <AX3>
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A; Residues: 1-271 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
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F;200-271/Domain: annexin repeat homology <AX4>
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                                                                                                                                                                                                                                                                                                Genetics:
Gene: At2g38760
                                                                                                                                                                                                                                                                                                                                                                                      Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 151;
                                                                                                                                                                                                                                                         position:
                                                                                          124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 MTLAKQBAKLVHEKIKOKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEBILKS-LEBG
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1 MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
                                                                                                                                 Similarity
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                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  UNIPROT:Q9ZVJ7; GB:AE002093; NID:g3785996; PIDN:AAC67342.1; GSPDB:G8
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                                                                                      Score 602.5; DB 2;
Pred. No. 4.7e-32;
6; Mismatches 123;
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Pred. No. 3.5
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PMID:10617197
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3.5e-43;
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probable annexin T23K23.6 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: B96704 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, S.; Huizar, L. A; Huthers, Huizar, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Fittle: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
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C;Genetics:
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A; Residues: 1-316 <STO>
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;Superfamily: annexin I;
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  TRGDYEKMLVALLG
                                                 AENSCFYFAKALRKSMKGLGTDDTALIRIVVTRAEVDMQFIITEYRKRYKKTLYNAVHSD
                                                                                                                                          RKHKSDDQTLIQIFTDRSRTHLVAVRSTYRSMYGKELGKAIRD-ETRGNFEHVLLTILQC
                                                                                                                                                                     DKHYNDED-VIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQC
                                                                                                                                                                                                                                                                                          ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
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A;Gene: GDB:ANXA13
A;Gene: GDB:ANXA13
A;Gene: GDB:ANXA13
A;Cross-references: GDB:9836021; OMIM:602573
A;Map position: 8q24.1-8q24.2
C;Superfamily: annexin I; annexin repeat homology
C;Superfamily: annexin intestine-specific #status experiments
F;2-316/Product: annexin intestine-specific #status experiments
F;17-88/Domain: annexin repeat homology cAX1>
F;28-44/Region: endonexin fold #status predicted
F;89-160/Domain: annexin repeat homology cAX2>
F;100-116/Region: endonexin fold #status predicted
F;772-244/Domain: annexin repeat homology cAX3>
F;184-200/Region: endonexin fold #status predicted
F;248-316/Domain: annexin repeat homology cAX4>
F;248-316/Domain: annexin repeat homology cAX4>
F;259-275/Region: endonexin fold #status predicted
F;24Modified site: myristylated amino end (Gly) (in mature forr
F;3/Modified site: aspartic acid (Asn) #status predicted
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J. Cell Biol. 116, 405-422, 1992
A;Title: A strategy for isolation of cDNAs encoding proteins
A;Reference number: A41733; MUID:92112982; PMID:1530946
A;Accession: A41733
A;Molecule type: mRNA
A;Molecule type: mRNA
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C;Genetics:
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Search completed: August 19, Job time : 41 secs
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Best Local Similarity
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Pred. No. 1.8e-25;
1; Mismatches 115;
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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US-08-526-136-4
US-09-949-016-7070
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US-08-948-276-1
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US-08-948-276-6
US-09-949-016-11534
US-08-948-276-1
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Sequence 62, Appl
Sequence 66, Appl
Sequence 65, Appli
Sequence 5533, Ap
Sequence 7952, Ap
Sequence 10475, A
Sequence 7621, Appli
Sequence 7621, Appli
Sequence 7621, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7070, Ap
Sequence 13, Appl
Sequence 7071, Ap
Sequence 10531, Appli
Sequence 11534, Appli
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RESULT

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GENERAL INFORMATION:

APPLICANT: Plinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting properties of INVENTION: death and their use in the FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-325-932A-66
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Best Local 9
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SOFTWARE: FastSEQ for
SEQ ID NO 66
LENGTH: 184
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant
FILE REFERENCE: 1022
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/325,932A CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pinus radiata
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TYPE: PRT
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                                                      61 LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH 120
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ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
                                                                                                      MSTIIVPVPIPTPSEDSERLRKAFEGWGTNEKSIIQILGHRTAAQRKVIRQSYFQLYEED
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Pred. No. 7.6e-77;
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the modification of forestry plant devel
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             GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES.
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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LENGTH: 323
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                                                                                                                                                                                                                                                                                                  Sequence 6593, Application US/09949016
Patent No. 6812339
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Best Local Similarity
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CURRENT FILING DATE: 1997-10-09
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TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
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SOFTWARE: PatentIn Vei
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OF SEQ ID NOS: 207012
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181 EQ 182
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Pred. No. 5.6e-38;
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PACENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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; ORGANISM: Human
US-09-949-016-7952
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                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7952
LENGTH: 334
                                                                                                                                                                                                     Query Match
Best Local Similarity
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SEQ ID NO 6593
LENGTH: 323
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Best Local
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                                                                                                                          APSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGEDLLKTLDKELSN
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                   HFEHLMVALVTPPAVFDAKQLKKSMKGAGTNEDALIEILTTRTSRQMKDISQAYYTVYKK 149
                                                       DFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLHARQAYHARYKK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EILCLRSFPQLKLTFDEYRNISQKDIVDSI-KGELSGHFEDLLLAIVNCVRNTPAFLAER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIKDKHYNDED-VI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPSVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAYGKELKDDLKGDLSG 78
                                                                                                    SPSVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAYGKELKDDLKGDLSG
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                                                                                                                                                                                 29.3%; Score 472; DB 4; Length 334; 36.3%; Pred. No. 5.9e-38; tive 63; Mismatches 130; Indels
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Pred. No. 5.6e-38;
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RESULT 8
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US-09-949-016-10475
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US-09-949-016-10475
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT PILING DATE: 2000-04-14
CRICK APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 112; Conservative
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TYPE: PRT
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Local Similarity 35.7%;
                                       303 DYEKMLVALLGEDD 316
                                                                                608 KPLFFADKLYKSMKGAGTDEKTLTRIMVSRSEIDLLNIRREFIEKYDKSLHQAIEGDTSG
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                                                                                                                                                              ETRFMTILCTRSYPHLRRVFQEFIKMTNYDVEHTIKKEMSGDVRDAFVAI----VQSVKN
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DFLKALLALCGGED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 461.5; DB 4;
Pred. No. 1.8e-36;
8; Mismatches 129;
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Length 557; Indels

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Gaps

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US-09-949-016-7621
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US-09-949-016-10476
                                                                                                                                                                                                                                                                                    Sequence 7621, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION FILE REFERENCE: CL001307
                   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 7621
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Best Local Similarity
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                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PRICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                           PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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    LENGTH:
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                                                 for Windows Version
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US-08-526-136-2
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US-09-949-016-7621
                                       APPLICATION NUMBER: 07/837,775
APPLICATION NUMBER: 07/847,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/0.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/214,036
APPLICATION NUMBER: US/08/214,036
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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ADDRESSEE: Fish & Richardson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
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Pred. No. 1,4e-35;
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RESULT 11
US-08-526-136-4
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                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.5)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
                                                        APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
APPLICATION NUMBER: 07/764,465
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Towle, Christine
TITLE OF INVENTION: ANNEXIN
NUMBER OF SEQUENCES: 36
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LENGTH: 503
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ADDRESSEB: Fish & Richardson
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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Local Similarity 36.0%; Pred. No. 1.6e-35;
nes 111; Conservative 57; Mismatches 132; Indels
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CITY: Boston
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RESULT 13
US-08-526-136-13
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SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 63
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 63, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Best Local Similarity 36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Composition: New York Title OF INVENTION: death (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                134 EEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 LEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIKDKHYNDEDVIR-
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                                                                                                                                                                   8 ORLVVLWSLDPAERDAYLANEATKRWTSSNQVLMEIACTRSPQQLLMARQAYHARYKKSL
                                                                                                EEDVAHHTTGDFRKLLVPLVSSYHYDGDEVNMTLAKAEAKILHE
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                                                                                                                                                                                                                                       27.9%; Score 449; DB 4; nilarity 80.8%; Pred. No. 2.1e-36; Conservative 11; Mismatches 9.
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t; Pred. No. 1.6e-35;
57; Mismatches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132; Indels
                                                                                                                                                                                                                                                                             Length 111;
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Application US/08526136

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY,AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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LENGTH: 466
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect (Version 5.0) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
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APPLICATION NUMBER:
FILING DATE: Februar
APPLICATION NUMBER:
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LLLAIVGQ 466
                                 MLVALLGE 314
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                                                                                                                                                                                                                                                DVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIKDKHYNDEDVIR-ILS 194
                                                                                                                                                                                                                                                                                   LILALEMPETYYDAWSLRKAMQGAGTQERVLIEILCTRTNQEIREIVRCYQSEFGRDLEK
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                                                                      FAERLYYAMKGAGTDDSTLVRIVVTRSEIDLVQIKQMFAQMYQKTLGTMIAGDTSGDYRR
                                                                                                       FVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDTRGDYEK 306
                                                                                                                                          TRSFPQLRATMEAYSRMANRDLLSSVSREFSGYVESG-----LKTILQCALNRPAF
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225 Franklin Street
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTMARE: FASTSEQ for Windows Version 4.
SEQ ID NO 7070
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US-09-949-016-7071
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US-09-949-016-7070
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                 CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                       Sequence 7071, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.7%; Score 447; DB 4; Length 467; Best Local Similarity 33.1%; Pred. No. 2.7e-35;
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TYPE: PRT
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FastSEQ for Windows Version
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SOFTWARE:

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; SEQ ID NO 7071
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7071
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Search completed: August 19, 2005, 20:28:18
Job time : 44 secs
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                                    307 MLVALLGE 314
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460 LLLAIVGQ 467
                                                                                       247 FVDVLRSAINKTGTDEGALTRIVTTRABIDLKVIGEEYQRRNSIPLEKAITKDTRGDYEK 306
                                                                                                                  400 FAERLYYAMKGAGTDDSTLVRIVVTRSEIDLVQIKQMFAQMYQKTLGTMIAGDTSGDYRR 459
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
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    1611
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US111A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*

21: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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1 MATLKVSDSVPAPSDDAEQL.....KDTRGDYEKMLVALLGEDDA 317
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-690-564-2
US-10-393-840-56
US-10-424-599-144032
US-10-425-114-47663
US-10-425-114-5802
US-10-219-220-22
US-10-393-840-114
US-10-219-220-260
US-10-219-220-260
US-10-424-599-213299
US-10-427-701-45089
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                                                    Sequence 2, Appli
Sequence 56, Appl
Sequence 14403,
Sequence 47663, A
Sequence 55802, A
Sequence 62, Appl
Sequence 114, App
Sequence 260, App
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-10-393-	-10-393-840-1	-10-219-	-10-424-599-2	-10-437-963-16944	0-425-115-2	-10-437-963-16943	-10-425-114-4	-10-437-963-	-10-393-840-5	-10-424-599-2	-10-424-599-211	-10-424-599-2	-10-739-930-92	0-425-	-10-425-114-59	-10-424-599-27984	-10-424-599-23	-10-424-599-17290	-10-424-599-2314	-10-393-840-1	-10-393-840-5	-10-219-220-65	0-425-114-4	-10-739-930-7820	-10-425-115-2483	-10-767-701-4610	0-437-963-	-10-425-114-4005	-10-437-963-18	-10-425-114-59	0-425-114-6	-10-425-114-64	-10-4
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ALIGNMENTS

RESULT 1

US-10-690-564-2

Sequence 2, Application US/10690564 Publication No. US20050089872A1 GENERAL INFORMATION:

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Best Local S
Matches 317
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CURRENT APPLICATION NUMBER: US/10/690,564
CURRENT FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: KOPATENTIN 1.71
SEQ ID NO 2
LENGTH: 317
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KOREA KUMHO PETROCHEMICAL CO., I
                                                                                                                                                               / Match 100.0%; Score 1611; DB 17; Local Similarity 100.0%; Pred. No. 1.5e-130; nes 317; Conservative 0; Mismatches 0;
121
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                                                                                                          ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK
                                                                    LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
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Sequence Sequence

213299, 45089, A 60631, A

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APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of plant Cell Wall
FILE REFERENCE: 11000.1012c3
CURRENT APPLICATION NUMBER: US/10/393,840
CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR FILING DATE: 1900-08-10
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/170,862
PRIOR APPLICATION NUMBER: US 09/148,426
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR APPLICATION NUMBER: DT NOSCONOMO PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR FILING DATE: 1999-10-08
                                     RESULT 3
US-10-424-599-144032
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US-10-393-840-56
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US-10-393-840-56
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Sequence 144032, Application US/10424599
Publication No. US20040031072A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 316
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Best Local Similarity
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71.9%;
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Pred. No. 7.8e-94;
88; Mismatches 50
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; FEATURE:
; OTHER INFORMATION: Clone
US-10-425-114-47663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-425-114-47663
                                                         APPLICANT: Kovalic, David K.
APPLICANT: Koreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 47663
LENGTH: 333
TYPE: PRT
ORGANISM: Glycine max
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APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 144032
LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 47663, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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26; Conservative
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71.3%;
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; OTHER INFORMATION: Clone ID: UC-GMROPIC033E01_FLI.pep
US-10-425-114-55802
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US-10-425-114-55802
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 55802
LENGTH: 333
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Best Local (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
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  ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
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                                                                                 ARKAYHVLYKKSLEEDVAHHTTGDFRKLILPLVSSYRYEGDEVNLTLAKTEAKLLHEKIS
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71.3%;
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Sequence 114, Application US/10393840
Publication No. US20030229922A1
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Cell Wall FILE REFERENCE: 11000.1012c3
CURRENT FILING DATE: 2003-03-0
CURRENT FILING DATE: 2003-03-0
PRIOR APPLICATION NUMBER: US 09/636,800
                                                                                                                                                                                               RESULT 7
US-10-393-840-114
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US-10-219-220-62
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SOPTWARE: FASTSEQ for Windows Version
SEQ ID NO 62
LENGTH: 316
TYPE: PRT
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Publication No.
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of
TITLE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
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nes 226; Conserv
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RESULT 8
US-10-219-220-260
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; Publication No.
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                                                                                                                                                 US-10-219-220-260
                                                                                                                                                            NUMBER OF SEQ ID NOS: 290

SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 260

LENGTH: 316

TYPE: PRT

ORGANISM: Eucalyptus grandis
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 114
LENGTH: 316
                                                                         Matches
                                                                                        Query Match
Best Local Similarity
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Best Local (
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of
FILE REFERENCE: 11000,1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. NO. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR FILING DATE: 1999-10-08
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                                                                                    70.3%; Score 1132.5; D 68.8%; Pred. No. 3e-89;
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US-10-424-599-213299
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SEQ ID NO 213399
LENGTH: 319
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Best Local Similarity
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APPLICANT: Kovalic David
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APPLICANT: Cao Yongwei
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OTHER INFORMATION: Clone
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OTHER INFORMATION: unsure at all Xaa locations
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NAME/KEY: unsure
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                       QCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAIT
                                                                                  KDKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLE-EGDDDDKFLALLRS-TI
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                                                                  AEKAYNDEELIRILSTRSKAQLTATLNQYINEFGNAINKDLKXELKKNVNICNLLRAXAI
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KCLTYPEKYFAKVLRLAINKLGTDEGALTRVVTTRAEVDLQRIAEEYQRRNSIPLDRAIA
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Pred. No. 1.6e.
45; Mismatches
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RESULT 11
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US-10-767-701-45089
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US-10-767-701-45089
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Publication No. US20040172684A1

GEMERAL INFORMATION:

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)8

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 45089

SEQ ID NO 45089

LENGTH: 314
                                                                                                                                                                                                                Sequence 60631, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
   APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Wolecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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Best Local Similarity
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                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 186841
LENGTH: 340
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LENGTH: 339
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                                                                                                                                                                                                                                         Query Match
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Best Local 9
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
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                                                                                                                                                                                                                    Local Similarity
121 ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
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                                       87 LLRSITDEISGDFERAVILWTLDPAERDAVLANEAARKWKPGNRVLVEIACTRTSAQIFA 146
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RESULT 14
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Sequence 60513, Application US/10425114
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Best Local Similarity
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LENGTH: 361
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT FILING DATE: 2003-04-28
UNMBER OF SEQ ID NOS: 73128
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ORGANISM: Zea mays
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                                                                                          SGDYESMLLALLGQE 361
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Pred. No. 1.5e-78;
53; Mismatches 70; I
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                            APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 59289

LENGTH: 344

TYPE: prm
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US-10-425-114-59289
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SEQ ID NO 60513
LENGTH: 341
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                  TYPE: PRT
ORGANISM:
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

C -!- SIMILARITY: Belongs to the annexin family.

C -!- SIMILARITY: Contains 4 annexin repeats.

REMBL; AP083913; AAD34236.1; -.

REMBL; AP083913; AAD34236.1; -.

REMBL; AV086570; AAM63633.1; -.

REMBL; AV086570; AAM63633.1; -.

REMBL; AP032435; AAG48798.1; -.

REMBL; AP032435; AAG29977.1; -.

REMBL; BT003359; AAG29977.1; -.

REMBL; BT003599; F:calcium ion binding; IEA.

GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.

GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.

REMBL; AP089118; Annexin; 4.

REMBL; AP089118; ANNEXIN; A.

REMBL; SM00335; ANX; 4.

REMBL; SM00335; ANX; 4.

REMBL; SM00335; ANNEXIN; 1.

ANNEXIN; Calcium-binding; Calcium/phospholipid-binding; GW Repeat.
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SEQUENCE
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X MEDLINE=97008169; PubMed=8855345; DOI=10.1073/pnas.93.20.11268;

X MEDLINE=97008169; PubMed=8855345; Kush A.K.;

Gidrol X., Sabelli P.A., Fern Y.S., Kush A.K.;

A Gidrol X., Sabelli P.A., Fern Y.S., Kush A.K.;

A Gidrol X., Sabelli P.A., Fern Y.S., Kush A.K.;

A Gidrol X., Sabelli P.A., Fern Y.S., Kush A.K.;

T mutant of Escherichia coli from H202 stress.";

Proc. Natl. Acad. Sci. U.S. A. 93:11268-11273(1996).

C -!- SIMILARITY: Belongs to the annexin family.

C -!- SIMILARITY: Contains 4 annexin repeats.

R EMBL; U28415; AAC49472.1; -.

R H3SP; P93157; 1N00.

R GO; GO:0005504; F:calcium ion binding; IEA.

R GO; GO:0005504; F:calcium-dependent phospholipid binding; IEA.

R InterPro; IPR001464; Annexin.
Q39001;
Q39001;
01-NOV-1996
01-NOV-1996
01-MAR-2004
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Q1-FEB-1997
Q1-FEB-1997
Q1-CCT-2003
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PRINTS; PR00196; ANNEXIN.
PRODOM; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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(TrEMBLrel. 25, Last annotation update)
                                                                                                          PRELIMINARY;
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NON TER
SEQUENCE
                                                                                         Brassica juncea (Leaf mustard) (Indian mustard).

Brassica juncea (Leaf mustard) (Indian mustard).

Bukaryota; Viridiplantae; Streptophyta; Brabryophyta; Tracheop
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots;

eurosids II; Brassicales; Brassicaceae; Brassica.
  SEQUENCE FROM N.A. TISSUE=Floral bud;
                                                  NCBI_TaxID=3707;
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PRINTS; PRO1814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4
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InterPro; IPR009118; Annexin plant.
Pfam; PF00191; Annexin; 4.
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Schantz R., Schantz M.L., Ho
Submitted (JUL-1996) to the
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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-!- SIMILARITY: Contains 4 annexin repe
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Pred. No. 3.2e
2; Mismatches
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Best Local S
Matches 289
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"Annexin cDNA from the floral bud of Brassica jun Submitted (JUL-2003) to the EMBL/GenBank/DDBJ dat -!- SIMILARITY: Belongs to the annexin family. -!- SIMILARITY: Contains 4 annexin repeats. EMBL; AY356355; AAR10457.1; -. InterPro; IPR001464; Annexin. InterPro; IPR009118; Annexin_plant. Pfam; PF00191; Annexin.
01-NOV-1998
01-NOV-1998
01-MAR-2004
                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; eudicotyle
eurosids II; Malvales; Malvaceae; Malvo
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SEQUENCE
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Gossypium hirsutum (Upland
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PRINTS; PR01814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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Pred. No. 1.6e
22; Mismatches
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RESULT
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Best Local 9
pDB; 1N00; X ray; A=1-315.

GO; GO:0005509; F:calcium ion binding; IE
GO; GO:0005544; F:calcium-dependent phosp
InterPro; IPR001464; Annexin.
InterPro; IPR009118; Annexin plant.
Pfam; PF00191; Annexin; 4.
PRINTS; PR00196; ANNEXIN.
PRINTS; PR01814; ANNEXINPLANT.
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SEQUENCE
                                                                                                                                                                                 -!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
EMBL; U73746; AAB6793.2; -.
ETR; T10805, T10805.
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STRAIN-Acalá SJ-2; TISSUE-Cotton:
MEDLINE-97374485; PubMed-9230934;
Delmer D.P., Potkha T.S.;
"Structures and functions of anne:
Cell, Mol. Life Sci. 53:546-553(1)
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01-OCT-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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PRINTS; PRO1814; ANNEXINPLANT.
PRODOM; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                      functions of annexins in plants."; Sci. 53:546-553(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Upland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36002 MW;
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73.5%;
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Pred. No. 2.8
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                                                                                                                     phospholipid
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Best Local S
Matches 229
        response to low temperature.";

plant Cell Physiol. 41:177-184 (2000).
-!- SIMILARITY: Belongs to the annexin fa
-!- SIMILARITY: Contains 4 annexin repeat
EMBL; AF006197; AB71830.1; --
HSSP; P93157; 1N00.
GO; GO:0005509; F:calcium ion binding; IE;
GO; GO:0005544; F:calcium-dependent phosp)
                                                                                                                                                                                                                                                                                                                                                                                         022341;
                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Leaves without petioles;
Vazquez-Tello A., Uozumi T.;
"Cloning and characterization of a Lavatera thuringiaca cDNA an annexin whose expression is stimulated by low temperature.
Plant Physiol. 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat.
                                                                                                                                                                                                                                                                               Spermatophyta; Magnoli eurosids II; Malvales;
                                                                                                                                                                                                                                                                                                    Lavatera thuringiaca.
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                             Annexin.
Name=AnxLt1;
                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998
01-JAN-1998
                                                                                                         Breton G., Vazquez-Tello A., Danyluk J., "Two novel intrinsic annexins accumulate
                                                                                                                               TISSUE=Leaves without petioles; MEDLINE=20255875; PubMed=10795312;
                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004
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Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                  NCBI_TaxID=61660;
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                                                                                                                                                          SEQUENCE FROM N.A.
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IPR001464;
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alvales; Malvaceae;
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73.48;
Annexin
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yta; eudicotyledons; core eudi
lvaceae; Malvoideae; Lavatera
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Last sequence update)
Last annotation update)
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Pred. No. 1e-67;
   binding; IEA.
endent phospholipid
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wheat
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           binding;
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membranes
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Best Local Sim
Matches 225;
PIR; S66274; S66274.

PDB; 1DK5; X-ray; A/B=1-314.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005504; F:calcium-dependent phospholipid |
InterPro; IPR001464; Annexin.
InterPro; IPR009118; Annexin.
Pfam; PF00191; Annexin; 4.

PRINTS; PR00196; ANNEXIN.

PRINTS; PR01814; ANNEXINPLANT.
                                                                                                                                                        MEDLINE=96198603; PubMed=8925897; DOI=10.1016/0014-5793(96)00252-9; Proust J., Houlne G., Schantz M.L., Schantz R.; "Characterization and gene expression of an annexin during fruit development in Cappicum annuum."; FEBS Lett. 383:208-212(1996).
                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster lamiids; Solanales; Solanaceae; Capsicum.
                                                                                                                  -!- SIMILARITY: Belongs to the annexin repe emBL; X93308; CAA63710.1; -.
                                                                                                                                                                                                                                                                                                                                            01-NOV-1996
01-MAR-2004
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SEQUENCE
                                                                                                                                                                                                                           TISSUE=Fruit;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              NCBI_TaxID=4072;
                                                                                                                                                                                                                                                                                                                 Capsicum annuum (Bell pepper).
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                                                                                                                                                                                                                                                                                                                                                                                                 Q42657
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Annexin; Calcium, Calcium-binding; Calcium/phospholipid-binding;
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PRINTS; PR01814; ANNEXINPLANT
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Pfam; PF00191; Annexin; 4.
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SM00335; ANX; 4.
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71.0%;
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26,
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Pred. No. 1.9e
43; Mismatches
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                                                                                                                                            family.
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01-MAY-2000
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SEQUENCE
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GO; GO:000554; F:calcium-dependent phospholipid
InterPro; IPR001464; Annexin.
InterPro; IPR009118; Annexin plant.
Pfam; PF00191; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
EMBL, AJ130829; CAA10210.1; -.
HSSP; Q42657; 1DK5.
30; CO.nonero
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Eukaryota; Viridiplantae; Eteptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
lamiids; Solanales; Solanaceae; Capsicum.
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SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding;
                                                                                                                                      PRINTS; PR00196; ANNEXIN.
PRINTS; PR01814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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Submitted (DEC-1998) to the
                                                                                            PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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les 212; Conserv
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Last annotation update)
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Pred. No. 6.6e
58; Mismatches
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    Score 1112.5;
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edons; core eudicots; aster
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Matches 211; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Proust J., Houlne G., Schantz M.L., Schantz R.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Helongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
EMBL; AJ130956; CAA10261.1; -.
HSSP; P93157; 1N00.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding
InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                             Repeat.
SEQUENCE
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ProDom; PD000143; Annexin
SMART; SM00335; ANX; 4.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

lamiids; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium, Calcium-binding; Calcium/phospholipid-binding;
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Annexin P38.
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                                                                                               MASLKVPASVPDPCEDAEQLKKAFKGWGTNEELIIQILAHRNAAQRKLIRDSYAAAYGED
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                                                                                                                                                                                                                                                                                          316 AA;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                          Score 1109.5; DB 2; Pred. No. 2.1e-62; 7; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
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RESULT
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                                                                                                                                                              Query Match
Best Local S
Matches 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P93158 PRELIMINARY;
P93158;
01-MAY-1997 (TrEMBLrel. C
01-MAY-1997 (TrEMBLrel. C
01-MAR-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Physiol. 113:305-305(1997).

-!- DOMAIN: A pair of annexin repeats may form
-calcium and phospholipid (By similarity).
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
EMBL; U73747; AAB67994.1; -.
PIR; T10807; T10807.
PIR; P93157; 1N00.
                                                                                                                                                                                                                                                                               Repeat.
                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0196; ANNEXIN.
PRINTS; PRO1814; ANNEXINDLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potikha T.S., Delmer D.P.; "cDNA Clones for Annexin AnnGh1 (Accession No. (Accession No. U73747) from Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Acala SJ-2; MEDLINE=97161127; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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Name=AnnGh2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium hirsutum (Upland
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00191; Annexin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001464; Annexin.
InterPro; IPR009118; Annexin_plant.
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                                                                                                                                                                                                                                                                                                                            Annexin;
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LKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLHA
                                                                                                                                                                                                                                                                                                                            Calcium; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                               PS00223; ANNEXIN; UNKNOWN
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                                                                                                    TLKVSDSVPAPSDDAE-QLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGEDL
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                                                                   TLKVPVHVPSPSEDAEWQLRKAFEGWGTNEQLIIDILAHRNAAQRNSIRKVYGEAYGEDL
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                                                                                                                                                                Conservative
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35834 MW;
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                                                                                                                                                              Pred. No. 3e-6
3; Mismatches
                                                                                                                                                                                   Score 1107; DB
Pred. No. 3e-62;
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                                                                                                                                                                                                                                                                                                                     _2.
_Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 214
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"Sequence Analysis of a Vacuole-Associated Annexin (Accession No. AF113545) (PGR99-028).";

Plant Physiol. 119:1147-1147(1999).

-i-SIMILARITY: Belongs to the annexin family.
-i-SIMILARITY: Contains 4 annexin repeats.
EMBL; AF113545; AAD24540.1;

HSSP; P93157; 1N00.
                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
Repeat.
SEQUENCE 316 AA; 35937 MW; 99E7973FC04C5FBE CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0196; ANNEXIN.
PRINTS; PRO1814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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InterPro; IPR009118; Annexin plant.
Pfam; PF00191; Annexin; 4.
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Seals D.F., Randall S.K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XEN8;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
                                                                                                                                LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
                                                                                                                                                                                                          MASLKVPTSVPEPYEDAEQLKKAFAGWGTNEALIIQILAHRNAAQRKLIRETYAAAYGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDYEKMLVALLGEDDA
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                                                                                                  LLKDLDAELTSDFQRAVLLWTLSPAERDAYLVNEATKRLTSSNWVILEIACTRSSDDLFK
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                                                                                                                                                                                                                                                                                                                                    Score 1106.5; DB Pred. No. 3.3e-62;
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316
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Best Local S
Matches 208
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024131;
01-JAN-1998
01-JAN-1998
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bight Yellow 2;

MEDLINE=99178786; PubMed=10080701; DOI=10.1023/A:1006199814795;

Proust J. Houlne G., Schantz M.L., Shen W.H., Schantz R.;

Proust J., Houlne G., Schantz M.L., Shen W.H., Schantz R.;

Regulation of biosynthesis and cellular localization of Sp32 annexins in tobacco By2 cells.";

in tobacco By2 cells.";

Plant Mol. Biol. 39:361372(1999).

-!- SIMILARITY: Belongs to the annexin family.

-!- SIMILARITY: Contains 4 annexin repeats.

EMBL; Y14972; CAA75213.1;

EMBL; Y17502; CAA76769.1;
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EMBL; Y17502; CAA76769.1;
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EMBL; Y17502; CAA76769.1;
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EMBL; Y17502; CAA76769.1;
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Eukaryota; Viridiplantae; Streptophyta; Embryc Spermatophyta; Magnoliophyta; eudicotyledons; lamiids; Solanales; Solanaceae; Nicotiana.
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PRINTS; PRO1814; ANNEXINPLANT.
PRODOM; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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InterPro; IPR009118; Annexin_plant.
Pfam; PF00191; Annexin; 4.
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Annexin; Calcium, Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=X511; Synonyms=an.1;
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181 DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
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                                                                     ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK
                                                                                                            LIKELDRELTNDFEKLVVVWTLDPSERDAYLAKEATKRWTKSNFVLVETACTRSPKELVL
                                                                                                                            LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
                                                                                                                                                                       MASLTVPAEVPSVAEDCEQLRSAFKGWGTNEKLIISILAHRNAAQRKLIQQTYAETFGED
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                                                                                                                                                                                                                                                                                               314 AA; 35855 MW;
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                                                                                                                                                                                                                                     Conservative
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                                                /AYHTTGEHPQLLVPLVSSYRYGGDEVDLRLAKAEAKILHEKIS
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                                                                                                                                                                                                                                                Score 1096.5;
Pred. No. 1.4e
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edons; core eudicots; aster
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SEQUENCE
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
EMBL; AJ401032; CAB92956.1; -.
HSSP; Q42657; 1DK5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00191; Annexin; 4.
PRINTS; PR00196; ANNEXIN;
PRINTS; PR01814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryc Spermatophyta; Magnoliophyta; eudicotyledons; Iamiids; Solanales; Solanaceae; Solanum.
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01-MAR-2004
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01-OCT-2000
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Annexin; Calcium, Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum tuberosum (Potato)
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InterPro; IPR009118; Annexin_plant.
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GO:0005544; F:calcium-dependent phospholipid binding;
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                           RGDYEKMLVALLGEDD
                                                                                                                    TRPELYFVDVLRSAINKTGTDEGALTRIVTTRABIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                                                                                                              DKHYNDEDVIRILGTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
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                                                                              VYPEHYFVEVLRDAINRRGTEEDHLSRVIATRAEVDLKTIANEYQKRDSIPLGRAIAKDT
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Pred. No. 1.4e-61;
6; Mismatches 47
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edons; core eudicots; asterids;
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InterPro; IPRO09118; Annexin plant.
PEAm; PP00191; Annexin; 4.
PRINTS; PR00196; ANNEXIN.
PRINTS; PR01814; ANNEXINPLANT.
PRODOM; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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O81536;
O1-NOV-1998
O1-NOV-1998
O1-MAR-2004
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Repeat.
SEQUENCE
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[2]
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
EMBL; AF079232; AAC97494.1; --
HSSP; Q42657; IDK5.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

lamiids; Solanales; Solanaceae; Solanum.
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Annexin; Calcium, Calcium-binding; Calcium/phospholipid-binding;
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"Blochemical characterization of tomato annexin calcium binding and phosphatase activities.";
J. Biol. Chem. 273:34920-34925(1998).
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Lim E.K., Roberts M.R., Bowles D.
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GO; GO:0005544; F:calcium-dependent phospholipid binding;
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                                                                              TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
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                                                   VYPEHYFVEVLRDAINRRGTBEDHLTRVIATRAEVDLKTIANEYQKRDSVPLGRAIAKDT
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7; Mismatches
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Search completed: August 19, 2005, 20:46:32 Job time : 182 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USTO_spcol/US10690564/runat 19082005 172307 25292/app_query.fasta_1.455
-Q=/cgn2 1/USTO_spcol/US10690564/runat 19082005 172307 25292/app_query.fasta_1.455
-DB=GenEmbl -QFMT=fastap -SUFFIX-srge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLENO -MAXLEN=2000000000
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-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSTBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                             Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                             Score
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Ygapop 10.0 , X
Fgapop 6.0 , E
Delop 6.0 , E
                                                           Match
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                                                                          Query
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Copyright (c) 1993 - 2005 Compugen Ltd.
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BT003359 Arabidops
AY086570 Arabidops
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019236	B01923	œ	81494	•	877
88832	AF188832	œ	9	•	879
5 2	ZMANNP35	œ	1257	•	949.5
787	AK101787	œ	1223		981.5
8	AY014798	œ	1003	•	982.5
2	AK175892	œ	1120	٠	991.5
641	AK175641	ω	1120	•	991.5
72	AK175572 ·	ω	1120	•	991.5
559	AK072559	œ	1274	٠	004.5
44 Z.	ZMANNP33	ω	1277	•	009.5
4799	AY014799	œ	1005	•	019.5
_	AY070400	œ	1230	•	1067
AY085713 Arabidops	AY085713	œ	1160	66.2	1067
_	AF083914	æ	1137	•	1067
~	AY096577	œ	985	•	1067
_	CQ806274	9	954		1067
1. sativa	MSANN	œ	1182	•	067.5
-	AF079231	œ	1242	•	1080
	NTANNE671	œ	1172	•	087.5
AY351650 Gossypium	AY351650	œ	1086	•	093.5
	AF079232	œ	1160	•	095.5
Y14972 Nicotiana t	NTANNES11	œ	1196	•	096.5
Solanum	STU401032	œ	945	•	096.5
AF113545 Nicotiana	AF113545	œ	1197	68.7	106.5
AX927134 Sequence	AX927134	σ	1157	•	106.5
U73747 Gossypium h	GHU73747	8	1146	68.7	1107
AJ130956 Capsicum	CAN130956	œ	1080	•	109.5
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	AR231102	σ	1293		171.5
	BD236034	σ	1293	72.7	171.5
	AF006197	œ	1112	٠	173.5
Material	BD236006	σ	2588	٠	185.5
Baypium	GHU73746	œ	948	•	193.5
	GHU89609	œ	1141	•	202.5
98 Sequenc	7	œ	81513	•	1450
	AY356355	œ	954		1507
X99224 A.thaliana	ATANNEX	œ	1206	•	549.5
415 Arabidopsi	841	8	1159	98.4	
083913 Arabidop	AF083913	œ	1230	٠	1611
723	234	8	1208	00	1611

ALIGNMENTS

Alignment Scores: Pred. No.: Score: Percent Similarity:	ORIGIN	FEATURES	TITLE JOURNAL	REFERENCE AUTHORS		ORGANISM	KEYWORDS	VERSION	DEFINITION	TOCUS C0806050	1
Scores: 8.28e-129 Length: 954 : 1611.00 Matches: 317 Lmilarity: 100.00% Conservative: 0			Identification of novel e2f target genes and use thereof Patent: NO 2004035798-A 2461 29-APR-2004; CropDesign N.V. (BB)	<pre>1 Inze,D., de Veylder,L. and Vlieghe,K.</pre>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotytledona; core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.		Brabidoneia thaliana (thale creec)	CQ806050.1 GI:47111659		CQ806050 954 bp DNA linear PAT 10-MAY-2004	

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TITLE
JOURNAL
REFERENCE
AUTHORS
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Arabidopsis thaliana (thale CLESD),

Arabidopsis thaliana

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.

Tosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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3 (bases 1 to 954)

Yamada,K., Dale,J.M., Hsuan,V.W., Onodera,C.S., Quach,H.L.,
Yariumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R.
Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R.
Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A
Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.
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Direct Submission
Submitted (28-DEC-2000) Plant
Submitted (28-DEC-2000) VIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-MAY-2003) Plant Gene Expression Street, Albany, CA 94710, USA Annotation based on July 2002 version of the A submitted to Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H., Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R.
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Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L.,
Yamada, K., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R.,
Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R.,
Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A.,
Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theologis,A.
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                                                                                                                                                                                                                                                     /translation="MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAE
GRKVIRQAYHETYGEDLLKTLDKELSNDFERAILLWTLEFGERDALLANEATKRWTSS
NQVLMEVACTRTSTQLLHARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEG
DEVNMTLAKQEAKLVHEKIKDKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILK
SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C00123
                                                                                                                                                                                                                                LKVIGEEYQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                          annexin'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="This clone is now in pUNI 51 vector.
it was in pUNI-T3-D/V5-His-TOPO under the c
                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAG48798.1"
/db_xref="GI:12083278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=experimental
/product="putative Ca2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="At1g35720"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:3702"
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Tang, C.C.,

Dale, J.M.,

CA 94304,

Tripp, M., Lee, J.M., Ecker, J

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RESULT 3
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   ACCESSION
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                                 annexin (
BT003359
                                           BT003359
Arabidopsis thaliana Ca2+-dependent
Arabidopsin (At1g35720) mRNA, complete
                                                                                                                                                                                                                                                                                             ArgGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAspAspAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGluGluIleLeuLysSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members carried o sequencing and annotation of the RAFL CDNAs: Nguyen,M., Tri Southwick,A., Palm,C.J., Jones,T., Wu,T., Chen,H., Cheuk,R. Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Le Kim,C.J., Quach,H.L., Onodera,C.S., Shinn,P., Tang,C.C., Toroumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Ec Theologis,A. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (29-UAN-2003) DNA Sequencing and Technology
Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Southwick, A., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T., Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J., Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Lee, J.M., Ishida, J., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Onodera, C.S., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shinn, P., Tang, C.C. Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinoraki, K., Ecker, J., Theologis, A. and Davis, R.W.
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Arabidopsis thaliana (thale cress)
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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pENTR/SD-dTopo This is a clo clone RAFL06-11-P04 (AY072347)

cloned 347) as

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Matches:
Conservative:
Mismatches:
Indels:
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Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequencing of the Genset carried out the library production and sequencing of the fill-length clones. Ceres, Inc. carried out the clustering of the
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Arabidopsis thaliana (thale cress)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1208)
                                                                                                                                                                   AY072347
AY072347.1
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1208 bp rabidopsis thaliana Ca2+-dependent annexin (At1g35720) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                           ArgGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAspAspAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Salk, Stanford, PGEC (SSP) Consortium members carried ou sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C. Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Submitted (02-UAN-2002) DNA Sequencing and Technology
Stanford University, 855 California Avenue, Palo Alto,
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                   ArgSerAlaGluGlnArgLysValIleArgGlnAlaTyrHisGluThrTyrGlyGluAsp
                                                                                                                      ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis
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note="This clone i
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/chromosome="1"
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1 (bases 1 to 1230)
Clark,G.B. and Roux,S.J.
Isolation and Characterization of Two Different Arabidopsis CDNAs (Accession Nos. AF083913 and AF083914) (PGR 99-065)
Plant Physiol. 120 (1), 340 (1999)
2 (bases 1 to 1230)
Clark,G.B. and Roux,S.J.
                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Whitis, Austin, TX 78713, USA
Location/Qualifiers
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Submitted (06-JUN-1995) Anil K. Kush, Institute of Molecular & Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Republic of Singapore
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1159)

1 (bases 1 to 1159)

1 (Gidrol, X., Sabelli, P.A., Pern, Y.S. and Kush, A.K.

Annexin-like protein from Arabidopsis thaliana rescues delta oxyR mutant of Escherichia coli from H2O2 stress

Proc. Natl. Acad. Sci. U.S.A. 93 (20), 11268-11273 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. 97008169
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/db_xref="taxon:3702"
/clone="pOxy5"
/tissue_type="whole_seedling"
/clone_Tib="Lambda_UniZapII_cDN
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QRVJKRVACTRTSTQLLHARQAYHARYKKSLEEDVAHHTTGDERKLLVSILVTSYRYEK
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A.thaliana mRNA for annexin.
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X99224.1 GI:1429206
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Submitted (09-JUL-1996)
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Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae
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      LysThrLeuAspLysG1uLeuSerAsnAspPheG1uArgA1aI1eLeuLeuTrpThrLeu
                                                                         AlaGluGlnArgLysVallleArgGlnAlaTyrHisGluThrTyrGlyGluAspLeuLeu
                                                                                                                                      AlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHisArgSer
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                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA67608.1"
/brotein_id="CAA67608.1"
/db_xref="G1:1429207"
/db_xref="G0:1429207"
/db_xref="G0:1429207"
/db_xref="G0A;039001"
/db_xref="UniProt/TrEMBL:Q39001"
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KVIRQAYHETYGEDLLKTLDKELSNDFERAILLWTLEPGERRALLANEATKRWTSSNQ
VLMEVACTRTSTQLLHARQAYHARYKKSLEEDVAHTTGDFRKLVSLVTSYRYEGDE
VNMTLAKGEAKLVHEKKLKHYNDEDVIRILSTISKAQINATENRYQDDHTSYRYEGDE
VNMTLAKGEAKLVHEKKLKKHYNDEDVIRILSTISKAQINATENRYQDDHTSEBILKSL
EEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRABIDLK
VIGEEYQRRNSIPLRAITKDNCGDYGKMLVAIFGEDDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
|mol_type="mRNA"
|sub_species="ecotype Columbia"
|db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone
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2 (bases 1 to 954)
Jami, S. K. and Kirti, P.B.
Direct Submission
Submitted (30-UIL-2003) Department of Plant
Life Sciences, University of Hyderabad, Gach
Andhra Pradesh 500046, India
Location/Qualifiers
                                                                                                                                                                                                                                                                                             AY356355
Brassica
AY356355
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Brassica juncea
Brassica juncea
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Jami, S.K. and Kirti, P.
Annexin cDNA from the
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    GluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeu
                                             IleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGluGluIleLeuLysSerLeu
                                                                                                                                                                                              ACCACCGGTGACTTCAGAAAGCTTTTGGTTTCTCTTGTTAGCTCATACAGGTACGAAGGG
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                                                                                                                                                                                                                                                               AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgSerAlaGluGlnArgLysValIleArgGlnAlaTyrHisGluThrTyrGlyGluAsp
                                                                                   GACAAGCATTACAATGATGAAGATTTCATAAGGATTTTGTCCACAAGGAGCAAAGCACAG
                                                                                                                                                                                                                                                                                                       TCAAGCAACCAAGTGCTTATGGAAGTAGCTTGCACTAGGACCTCTACGCAGCTTCTTCAC
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Mismatches:
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Street, Albany, CA 94710,
4 (bases 1 to 81513)
                                                                                                                                                                                                                                                                                                                                              Street, Albany, CA 94
3 (bases 1 to 81513)
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                                                                                                                                                                                                                                                              Theologis, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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St., Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced gi:6693723.
The sequence is of BAC F14D7 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire
insert of this clone. It is shorter by 6954 bp because we submit
only the unique sequence of the clone. However, in order to
facilitate the joining of overlapping clones in the future for
creation of larger contigs, we provide small overlaps (200 bp)
between overlapping sumbitted clones. The 5' end of this sequence
overlaps by 200 bp to the 3' end of the sequence of the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 81513)

Liu,S.X., Chan,A., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Toriumi,M., Chin,C., Chiou,J., Choi,E., Chung,M., Gonzalez,A., Howng,B., Liu,A., Vaysberg,M., Altafi,H., Brooks;S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A., Theological and Yu, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-JAN-2000) Plant Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-JUN-2000) Plant Gene Expression Center,
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The sequence of BAC F14D7 from
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gb N96455, gb
gb R30014, gb
gb H36260, gb
gb H76134, gb
gb AA597533, 9
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                                                                                                                                                                                                                                                                                /note="Contains similarity to a putative protein CAB78009
gi|7267527 from Arabidopsis thaliana BAC T32A17
gb|AL161513. It contains Pumilio-family RNA binding
domains PF|00806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (7937. .8041,8115. 8757. .8919,9397. .10730))
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LKVIGEEYQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"
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join(5917. .5992,6589. .6734,6821. .7552)
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FGERFMGFGGFNGDFNFRGASDHRPLGSDGFLPSLDTNPFLKNHKSVEALDLCKKLHK
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MKVTEKCDVYSFGVLILELIIGKHPGDLVSSLSSSPGEALSLRSISDERVLEPRGQNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFGFCSHRRHTFLIYEYMEKGSLNKLLANDEEAKRLTWTKRINVVKGVAHALSYMHHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aliana gb|AF083913. It contains an annexin domain 100191. ESTS gb|H76460, gb|Z18518, gb|Z26190, N96455, gb|Z47714, gb|T41940, gb|T43657, gb|N95995, R30014, gb|T22046, gb|H37398, gb|H77008, gb|R29768, H36260, gb|Z17514, gb|W43175, gb|T76739, gb|AA712753, H76134, gb|T42209, gb|H36536, gb|A1998553, gb|Z32565, AA597533, gb|A11000145 and gb|A1100054 come from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .8364,8443.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(44612. 44780,45014. 45403,45501. 45644,45676. 466297. 46476,46633. 47029,47113. 47505,47737. 48082 48145. 48411,48465. 48541,48632. 48698) /gene="F14D7.6" /note="Strong similarity to a mutator-like transposase gi | 4063759 from Arabidopsis thaliana BAC T14A4 gb | AC005561."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F14D7.5"
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BAC T32M21 gb|AL162875. EST gb|AI994915 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CABIAIHRHGCCVLQCCISNSVGLQRERLVABISRNSLHLSQDPFGNYVVQYLIDQQV SAVKLLVQFRWHYABLATQKFSSHVLEKCLRKYPESRABIVRELLCVPNFEYLLQDPY ANYVIQTALSVTKGPVRAKLVAKVYRYGKLHSSPYCKKIFSKTILKK"
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NNNFHGVSPSPGEMRLLGRODSFNLNGFEEMLALKNHRDFLLDQIHEPIKRPPPFLRGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44612. .48698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(19422. .19496,19746. .19835,20053. .20194,
23655_ .23686))
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TCPWRVYATKLPDSDWFEVRSTTQTHTCSVDARGDFHKQASTVVIGKLMRTKYIGVGR

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30-AUG-1998

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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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                                              IleAspLeuLysValIleGlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLys
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                                                                                                                                                                                                                                           GAAATTCTCAAGAGTCTTGAGGAAGGAGGATGATGATGACAAGTTCCTTGCACTTTTGAGG
                                                                                                                                                                                                                                                                    GluIleLeuLysSerLeuGluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArg
                                                                                                                                                                                                                                                                                                                                           ThrargSerLysAlaGlnIleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                           GTCCATGAGAAAATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                ValHisGluLysIleLysAspLysHisTyrAsnAspGluAspValIleArgIleLeuSer 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerTyrArgTyrGluGlyAspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGACGTTGCTCACCACACTACCGGTGACTTCAGAAAGCTTTTTGGTTTCTCTTTGTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluAspValAlaHisHisThrThrGlyAspPheArgLysLeuLeuValSerLeuValThr 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerThrGlnLeuLeuHisAlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGlu 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaThrLysArgTrpThrSerSerAsnGlnValLeuMetGluValAlaCysThrArgThr 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAACCTACGGCGAAGACCTTCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGlnArgLysVallleArgGlnAlaTyrHisGluThrTyrGlyGluAspLeuLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGACTTGAAGGTCATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAA
                                                                                                                                                                    TCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGCTATCTTGTTGGACTCTTGAACCCCGGTGAGCGTGATGCTTTATTGGCTAATGAA 6880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgAlaIleLeuLeuTrpThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTOTTGACAAGGAGOTOTOTAACGATTTOGA-GGTTCGGTTTTCGGACTTTTAAGTATC 6760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPRANELRRMLRQDYALIQPYFKCLLETNPNSLVAMETEKDNSGVERFKYLFFALDAC
VQGYAYMRKVIVIDGTHLRGRYGGCLVAASAQDANFQVFPIAFGIVNSKNDEAWTWFM
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AUTHORS
TITLE
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Gossypium hirsutum
Gossypium hirsutum
Eusaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eusaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 1141)
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U89609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (13-FEB-1997) Botany,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Austin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shin, H. and Brown, R.M.Jr.
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EEVNMNLAKTEAKLLHEKISDKAYSDDDVIRVLATRSKQINATLNHYKNEYGNDINK
DLKADPKDEFLALLRSTVKCLVYPEKKYEKVLRLAINRRGTDEGALTRVVCTRAEVDL
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  GluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLysAsp
                                                                                                                                                                                                                                                       SerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHisAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGCGGAGCAACGAAACTTGATTCGAAAAACCTACGCTGAAACCTATGGAGAGGATCTC
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                                               ACTGGGGACTTCCATAAGCTCCTCCTACCTCTAGTGAGTTCATACAGATATGAGGGAGAG
                                                                                ThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGlyAsp
                                                                                                                                        AGGCAGGCTTATCATGCTCGTTATAAGAAGTCGCTTGAAGAGGACGTTGCTCATCACACG
                                                                                                                                                                ArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHisThr
                                                                                                                                                                                                                             CTTGATCCTGCAGGATGCCCTTTTGGCTAATGAAGCCACCAAAAGGTGGACTTCA
                                                                                                                                                                                                                                                                                                                                                LeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAB67993.2"
/db_xref="G1:15214410"
/db_xref="G1:15214410"
/translation="ayntypetypsysedceolrkapsgwgtnegllidilghrnaeq
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EVNMYLAKTEAALLHEKGISNRAYSDDDVIRYLATRSKAQINAYTLNHYKNEYGWDIKG
LKADPKDEFLALLRSTVKCLVYPEKYFEKVLRLAINERGTDEGALTRVVCTRAEVDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="evidence suggests that annexins may bind to an influence activity of callose synthase" /note="contains 4 repeats characteristic of other annexins; shows evidence of conserved calcium-binding domains; by comparison with other plant annexins as well as with the size of native cotton fiber annexin, this clone probably lacks 5'coding sequence for only the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal Met; calcium binding protein"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="21 days
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/tissue_type="cotton
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/product="annexin"
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420 141 360 81 180 61 120 60

21

Alignment Pred. No.: Score:	ORIGIN	FEATURES source			COMMENT	JOURNAL	REFERENCE AUTHORS	SOURCE	ACCESSION VERSION KEYWORDS	RESULT 13 BD236006 LOCUS DEFINITION	Qy Db	B &	D Qy	B 8	B &	B &	gg Qy	Db
Scores: 7.55e-92 Length: 2588 : 1185.50 Matches: 228	/mol_type="genomic una" /db_xref="taxon:71139"	FT	Mate	PF 08-CCT-1999 JP 2000575985 PR 13-CCT-1998 US 09/170862,11-AUG-1999 US 60/148426 PI LEONARD NATHAN BLOKSBERG PC C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/12,C12N15/00,C12N5/	Eucalyptus of 200252705 27-AUG-2002	PATENT: UP 2002527056-A 28 27-AUG-2002; GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLET FORESTS LTD	Spermatophyta; Magnollophyta; eudicotyledons; core rosids; Myrtales; Myrtaceae; Eucalyptus. 1 (bases 1 to 2588) Bloksberg, L. N. Materials and method for modification of plant coll	Eucalyptus grandis Eucalyptus grandis Eucalyptus grandis Eukaryota; Viridiplantae; Streptophyta; Embryo	6	4	302 GlyAspTyrGluLysMetLeuValAlaLeuLeuGly 313 ::: :::	282 GluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThrArg 301 :::	262 GluGiyAlaLeuThrArgileValThrThrArgAlaGluIleAspLeuLy8ValIleGly 281 	242 ArgProGluLeuTyrPheValAspValLeuArgSerAlaileAsnLysThrGlyThrAsp 261	222 GluGlyAspAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeuThr 241 :::	202 ASDAISThrPheASDAIGTYrGlDASDASDHISGlYGlUGlUIIeLeuLysSerLeuGlU 221	182 LysHisTyrAsnAspGluAspVallleArgIleLeuSerThrArgSerLysAlaGlnIle 201	
SULT 14	Qy 301 ArgGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAspAspAla 317	Oy 281 GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr 300	2107 ACTCGCCCTGAGAAGTATTTTGAAAAGGTTCTTCGTCTAGCCATCAATAAGCGAGGAACA 261 AspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysVallle	2050 AAAACTGATCCAAAAGACGCGTTCCTTACTATACTGAGAGCTACAGTAAAGTGCCTG 241 ThrArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThr	GluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeu	Qy 201 IleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGluGluIleLeuLysSerLeu 220	Oy 181 AspLysHisTyrAsnAspGluAspVallieArgIleLeuSerThrArgSerLysAlaGln 200	Qy 161 AspGluValAsnMetThTLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys 180	Qy 141 ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly 160	Oy 121 AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis 140	Oy 101 SerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHis 120	Qy 81 ThrieuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThr 100	Oy 61 LeuLeuLysThrLeuAspLysGluLeuSerAsnAspPheGluArgAlaileLeuLeuTrp 80 ::: :::	Oy 41 ArgSerAlaGluGlnArgLysValIleArgGlnAlaTyrHisGluThrTyrGlyGluAsp 60	Oy 21 ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis 40	Qy 1 MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu 20	6 -690-564-2 (1-317) x BD236006 (1-	Percent Similarity: 83.91% Conservative: 38 Best Local Similarity: 71.92% Mismatches: 50 Ouery Match: 73.59% Indels: 1

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Submitted (31-MAY-1997) Biological Sciences, Universite du Quebec,
Submitteal. C.P. 8888, Succ. Centre-Ville, Montreal, Quebec H3C 3P8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vazques-Tello,A. and Uozumi,T.
Vazques-Tello,A. and Uozumi,T.
Cloning and characterization of a Lavatera thuringiaca
Cloning and characterization of a Lavatera thuringiaca
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Lavatera.

1 (bases 1 to 1112)
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Breton,G., Vazquez-Tello,A.,
Two novel intrinsic annexins
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Vazquez-Tello, A. and Uozumi, T.
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 ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis
                                                                   MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu
                                                    ATGGCTACTCTTACAGTTCCCTCCACACTTCCGTCAGTGTCTGAAGATTGTGAACAACTC
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                                                                                                                                                                                                                                                                                                              /protein_id="AAB71830.1"
/db xref="G1:2459926"
/db xref="G1:2459926"
/translation="MATITUPSTLPSVSEDCEQLRKAPSGWGTNEDLIINILGHRNAD
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DEVMNTLAKTBAKLHEKISNKAYSDDDVIRVLATRSKSQINERLNHYKGMEYATDIK
DEVMNTLAKTBAKLHEKISNKAYSDDDVIRVLATRSKSQINERLNHYKGKEYATDIK
DLKADPKDEFLALLRSTVKCLVYPEKVIRKLAINKRGTDEGALTRVVSTRAEVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="AnxLt1"
/function="binds acidic phospholipids in a calcium-dependent manner"
/note="calcium-dependent, phospholipid binding protein; contains four characteristic repeats found in both anim
                                                                                                                                                                                                                                                                                               KIIADEYQRRNSVPLTRAIVKDTNGDYEKLLLVLAGEVEA"
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/tissue_type="leaves without
/note="from England"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 1293) Bloksberg, L.N.
Materials and method for modification of plant cell w
                                                                                                                                                                                BD236034
Materials and method
                                                                                    Pinus radiata (Monterey pine)
Pinus radiata
                                                                                                                JP 2002527056-A/56
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GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE FORESTS LTD

OS Pinus radiata (radiata pine)
PN JP 2002527056-A/56
PD 27-AUG-2002
PF 08-CCT-1999 UP 2000575985
PR 13-OCT-1998 US 09/170862,11-AUG-1999 US 60/148426 PI LEONARD NATHAN BLOKESBERG
PC C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/12,C12N15/00,C12N5/PC 00

CC Materials and method for modification of plant cell wall CC
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GAGAAGGCTTATGGCCATGAGGATCTCATAAGGATTTTGGCTACTAGGAGCAAAGCACAG
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/mol_type="genomic DNA"
/db_xref="taxon:3347"
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-Q-/Cgn2 1/USPTO_spool/US10690564/runat 19082005_172306_25282/app_query.fasta_1.455
-DB=N_Geneseq_16Dec04 -CpMT=fasta_p -SUPFIX=rng_-MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-sext -HEAPSIZE=500 -MINLEN=2000000000
-USER=US10690564_@CGN_1_1_470_@runat_19082005_172306_25282 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                           Score
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New lipid metabolism proteins and nucleic acids, useful transgenic plants with increased levels of seed storage lipid, a fatty acid, a starch or a seed storage protein.
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                             Claim
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P-PSDB; ADN74567.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function a transcription factors. This polynucleotide sequence is thale cress cDNA repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa transcription factor, given in an exemplification of the invention.
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                          ThrArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThr
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                                                                                                                     IleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGluGluIleLeuLysSerLeu
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                                                                                                                                                                                                 GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCT
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                                                                                                                                                                                                                                                                                                      AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
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              ACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGGAACT
                                                         GAGGAAGGAGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTGCTTG
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RESULT 4
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                                                                                                      GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr
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                                                                                           GGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTTGGAGAAAGCTATTACCAAAGACACT
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                           pLeuLeuLysThrLeuAspLysGluLeuSerAsnAspPheGluArgAlaIleLeuLeuTr
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                                                                                                                                                    07-MAY-2001; 2001US-00849529
12-DEC-2001; 2001US-00021323
  Kovalic
                                                (KOVA/)
(ZHOU/)
(CAOY/)
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New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                                         WPI;
Claim 1; SEQ ID NO 4242; 14pp; English
                                                                                                                                                                                                                                                         2004-667718/65
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invention relates to a recombinant polynucleotide comprising any

comprises transforming a plant having an improved property. Producing a plant having an improved property comprises transforming a plant with a recombinant construct comprising a coding sequence for a polypeptide associated with the property, and growing the transformed plant. The polypeptide is couseful for improving plant cold tolerance, manipulating growth rate in the property, and growing the transformed plant. The polypeptide is colding increased resistance to plant disease, conducing galactomannan (or lignin or plant growth regulators), improving plant tolerance, providing increased resistance to plant disease, conducing galactomannan (or lignin or plant growth regulators), improving plant tolerance to extreme osmotic conditions or to pathogens or peste, improving yield by modification of photosynthesis, modifying seed oil or protein yield complete the and/or content, improving yield by modification of photosynthesis, modifying seed oil or protein yield constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, in physical arrays of molecules, as plant breeding markers, constructs, providing the providing physical arrays of molecules, as plant breeding markers, constructs, providing physical arrays of mo the 58798 Cotton plant cDNA sequences mentioned in the specification. Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having Ģ, an

Sequence 1184 BP; 375 A; 233 C; 281 G; 295 Ŧ; 0 U; 0 Other;

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Query
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                               US-10-690-564-2 (1-317) x ADR63461 (1-1184)
                                                                 Best Local
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SerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHis
                                                                            ThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThr
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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences given in Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16286 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the
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present invention
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: 8.78e-11 1185.50 83.91% 71.92% 73.59% .78e-110 Length:
Matches:
Conservative:
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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (B) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are
                                                                                                                                                                                                                                                                                                                                  New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.
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                                                                                                                                                                                                                        The present invention relates to coding sequences (see AAF44740-F44840 and AAF44843-F44844) and proteins (see AAB65714-B65814) involved in programmed cell death (PCD; appotosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant
                                                                                                                                                                                                                                                                                                                                               Novel defender against cell death polynucleotide useful for modulating programmed cell death pathway and specific development pathways in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF44756 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide useful altering the development cycle of plant development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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GCAAGACAAGCATATCATGCCCGATACAAGAAGTCAATGGAAGAGGGACGTCGCTCACCAC
              AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
                                                                                                                                                                     AGGAATGCCGCCAGAGGAAGCTGATTCCGCCAAACCTATGCCGAGACTTACGGCGAGGAC
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programmed cell death; plant development; plant cell cycle; ATL2; DAD1; Dnase; lls; lsd1; nucellin-like aspartic protease; annexin; prohibitin; fen-like protein; rac2; retinoblastoma-related protein; SINA; TFIID; TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like protein; gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1; defender against cell death; lethal leaf spot; lesion stimulating death, seven in absentinia; transcription initiation factor;
                                                                                          04-JUN-1999;
                                                                                                                                       14-AUG-2002;
                                                                                                                                                                                                                                                                        Eucalyptus grandis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotide sequence that is one of 145 fully defined sequences of 221-3415 base pairs (bp), given in the specification, and/or its complements, reverse complements, reverse sequences, or sequences having 75, 90 or 95 $ sequence identity to or that hybridise under stringent hybridisation conditions to one of the 145 sequences. The methods and compositions of the present invention to do with (I) are useful for modulating programmed cell death and thereby altering the development cycle of plant cells, and altering plant development. This sequence encodes a protein associated with the programmed cell death pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide useful for modulating programmed cell death, altering the development cycle of plant cells, and subsequently modifying
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The present invention describes a method for identifying and validating plant genes/proteins as targets for agrochemicals comprising determining the expression profiles of a plant and downregulating the expression of the gene or protein in the plant or plant cell. Also comprising the use of the above method or the use of any of the 785 fully defined nucleotide sequences (ADF37942 to ADF38726) or protein sequences, or their homologues, functional fragments or derivatives; (2) a method for producing an agrochemical resistant plant, comprising the use of the above mentioned nucleotide or protein sequences; (3) an isolated nucleotic acid that is identified by any of the above methods or that comprises at least a part of a nucleic acid sequence chosen from any of the 785 nucleotide sequences given in the specification; (4) a plant tolerant to an agrochemical, in which the expression level of one or more of the nucleic acid sequences given in the specification is modulated; and (5) a harvestable part of the plant described above. The method is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying and validating plant genes or proteins as targets for agrochemicals, useful for producing agrochemical-resistant plants, comprises determining and down regulating the gene or protein expportiles of a plant.
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15-JUL-2002; 2002US-0396124P.
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                                                    CC This invention relates to a novel method for altering one or more plant CC characteristics. Specifically, it refers to identifying genes that are up CC - or down-regulated in transgenic plants overexpressing the heterodimeric CC E2Fa/DPa transcription factor of Arabidopsis and using these sequences to CC generating transgenic plants for the production of growth regulators, CC enzymes, therapeutics, pharmaceuticals and animal feed products, where CC the altered plant characteristics are selected from increased yield or CC biomass, enhanced survival capacity, stress tolerance, plant architecture CC or physiology, altered endoreduplication, biochemistry, signal CC transduction, storage lipid mobilisation and/or altered photosynthesis, CC each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers CC during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polymucleotide sequence is thate cress cDNA repressed 1.3 fold or more in plants overexpressing the E2Fa/DPa transcription factor, given in an exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ss; plant; transgenic; E2Fa/DPa transcription factor;
growth regulator; animal feed product; thale cress;
cell wall biosynthesis; nitrogen metabolism; carbon metabolism
Sequence
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중 음 성

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Search completed: August 22, 2005, 10:30:32 Job time: 677 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-O=/GGPA_I/USPTO_Spool/US10690564/runat_19082005_172307_25304/app_query.fasta_1.455
-OB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DB=EST -QFMT=fastap -SUFFIX=rst -MAYRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
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-DEV_TIMEOUT=120 -WARN_INEGUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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ALIGNMENTS

	COMMENT	October	TITLE	AUTHORS	REFERENCE	JOURNAL.		TITLE			AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION			DEFINITION	LOCUS	RESULT 1 CNSOABR2
Life Technologies (a division of invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,	Web: www.genoscope.cns.fr) The sequences are based on single pass reads.	BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr	Direct Submission Submission Contro National de Semiencade :	Genoscope.	2 (bases 1 to 1095)	Unbub] ished	A Combined Approach to Evaluate and Improve Arabidopsis Genome	Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:	Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.	Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,	Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,	1 (bases 1 to 1095)	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arabidopsis thaliana	Arabidopsīs thaliana (thale cress)	HTC; GSLT cDNA.	BX816579.1 GI:42471684	BX816579	Arabidopsis thaliana (thale cress).	GSLTPGH56ZG07 of Hormone Treated Callus of strain col-0 of	Arabidopsis thaliana Full-length cDNA Complete sequence from clone	CNSOABR2 1095 bp mRNA linear HTC 06-FEB-2004	

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Query Match:
DB:
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URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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IleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGluGluIleLeuLysSerLeu
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                                                                                          AspLysHisTyrAsnAspGluAspVallleArgIleLeuSerThrArgSerLysAlaGln
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BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr)
Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). S prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
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  /tissue_type="Hormone Treated Callus"
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                                                                 clone="GSLTPGH18ZF02"
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                                                                                         Similarity:
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Pull
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1 (bases 1 to 1155)
1 (Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Castelli, V., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
Mhole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
Machine Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                               /strain="col-0"
/db xref="taxon:3702"
/clone="GSLTSIL62E06"
/tlssue_type="Silique"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis
/mol_type="mRNA"
                                                                                                                                                                                                                                                      /gene="At1g35720"
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                                                                 LNSU9Y3M 1034 bp mRNA linear HTC Arabidopsis thaliana Full-length cDNA Complete sequence GSLTLS23ZB01 of Adult vegetative tissue of strain col-0 Arabidopsis thaliana (thale cress).
Arabidopsis
                  BX841810.1 GI:42454468
HTC; GSLT_cDNA.
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                                                                                                                                                                                                              rargGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAspAspAla 317
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INNA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
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1 (bases 1 to 1034)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Direct Submission
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ACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTACAAAGAGATGGACT
                  ThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThr
                                                                           CTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCTTGTTGTGG
                                                                                                LeuLeuLysThrLeuAspLysGluLeuSerAsnAspPheGluArgAlaIleLeuLeuTrp
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/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSLTLS23ZB01"
/tissue_type="Adult veg
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At1g35720"
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                                                                                                                                                                                                                           Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weisshaar, B.

Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thal Genome Res. 13 (6), 1250-1257 (2003)
                                                                  Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding
Carl-von-Linne Weg 10, 50829 Koeln, Gern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CF652924 910 bp mRNA linear EST 85-L020135w-066-001-IZ1-SP6P MPIZ-ADIS-066 Arabidopsis t Cione MPIZp2001I211Q 5-PRIME, mRNA sequence.
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 910 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosida; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 910)
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                                                    ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
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                                                                                                                                                      AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
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//lab.host="E. coli TOP10"
//clone lib="MMPIZ-ADIS-066"
//clone lib="MMPIZ-ADIS-066"
//note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: Not1;
//note="Vector: pCMVSPORT6; Site 3: Not2; Sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="root"
/lab_host="E. coli 1
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Arabidopsis thaliana
Eukaryota; Viridiplancae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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BX838972
thaliana
                                                                                                                                                                                                   genome released by MIPS (Munich Information center f Sequences).
                                                                                                                                                                                                                                           The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Cas V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schacher V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidops
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRAN
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.
                                                                                                                                        http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
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Unpublished (2004)
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Arabidopsis thaliana Flowers and buds Col-0 Arabidopsis
cDNA clone GSLTFB50ZD03 5PRIM, mRNA sequence.
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                                       /ecotype="Col-0"
/db_xref="taxon:3702"
                                                                             organism="Arabidopsis"
/mol_type="mRNA"
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                         AAGATGCTCGTCGCACTTCTCGGTGAAGATGATGCT
                                                LysMetLeuValAlaLeuLeuGlyGluAspAspAla
                                                                                                                         ArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThrArgGlyAspTyrGlu
                                                                                                                                                                                    ACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGGAGTACCAG
                                                                                                                                                                                                           ThrArgIleValThrThrArgAlaGluIleAspLeuLysValIleGlyGluGluTyrGln
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
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Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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0-1020580-066-004-L08-SP6P MPIZ-ADIS-066 Arabidopsis thaliana cDNA
clone MPIZp2001L084Q 5-PRIME, mRNA sequence.
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                                          MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu
                          ATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCAATTG
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Length: 843 Std Error: 0
                                                                                                                                                                                                                                                                                                                                              compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wassilewskija-0; roots from three weeks old plants grown on MS-plates at 26M-0C with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sall-NotI, primer sites and orientation:

SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; GATEWAY
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/clone="MPIZp2001L084Q"
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/tissue type="root"
/lab_host="E. coli TOP10"
/clone_1ib="MPIZ-ADIS-066"
/clone_1ib="MPIZ-ADIS-066; Site_1: SalI; Site_2: Not1;
/note="Vector: pcMVSPORT6; Site_1: SalI; Site_2: Not1;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Tosida; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S.
and Welinder,K.G.
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Contact: Karen G. Welinder
Institut for bioteknologi
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Sohngaardsholmsvej 4
Tel: +45 96358467
Fax: +45 98141808
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                                                                   AspLysHisTyrAsnAspGluAspVallleArgIleLeuSerThrArgSerLysAlaGln
                                                                                                                       AspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys
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  ATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAGTCTT
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library of Arabidopsis and E. cichoracearum infected
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
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/clone_lib="Infected Arabidopsis Leaf"
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                                                                                                                                                                                                               organism="Arabidopsis
                                                                                                        'gene="At1g35720"
9.68e-147
1327.00
99.62%
99.24%
82.37%
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Submitted (18-NOV-2003) Genoscope
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Location/Qualifiers
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/tissue_type="Hormone Treated Callus"
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Length:
Matches:
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(E-mail : segref@genoscope.cns.f)
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                                                      sequence.
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; triatiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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US-10-690-564-2 (1-317) x BU635010 (1-782)
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Fax: +45 98141808
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/db_xref="taxon:3702"
/dev_gtage="plant 3 weeks old, three days post infect
/dev_gtage="plant 3 weeks old, three days post infect
/clone lib="Infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
library of Arabidopsis and E. cichoracearum infected
from three weeks old Arabidopsis plants. Plants were
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12736302
Contact: Zhu,Y.
Contact Laboratory of Protein Engineering and Engineering
College of Life Sciences, Peking University
Beijing 100871, China
                                                                                                                       1 (bases 1 to 929)

Ji,S.J., Lu,Y.C., Feng,J.X., Wei,G., Li,J., Shi,Y.H., Fu,Q.,

Liu,D., Luc,J.C. and Zhu,Y.X.

Isolation and analyses of genes preferentially expressed during early cotton fiber development by subtractive FCR and cDNA array Nucleic Acids Res. 31 (10), 2534-2543 (2003)
                                                                                                                                                                                                                             Gossypium hirsutum (upland cotton)
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Gossypium hirsutum
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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/clone lib="cotton fiber subtracted cDNA library"
/note="The library was constructed using PCR-select cDNA
subtraction method with 10 dpa cotton fiber as tester an
fiberless mutant as driver"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://genome.arizona.edu
Plate: 03 row: B column: 10.
Location/Qualifiers
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Fax: 520 621 1259
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The University of Arizona
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Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Sod
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BCoRV; Library made by Invitrogen wIth RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80
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Contact: Rod A. Wing
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Fax: 520 621 1259
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GR Eb019H11.r GR Eb Gossypium raimondii cDNA clone GR Eb019H11
3', mRNA sequence.
CO116938.1 GI:48815625
EST.
Gossypium raimondii
Gossypium raimondii
Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicote; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

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Plate: 019 row: H column: 11.
Location/Qualifiers
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Contact: Rod A. Wing
Arizona Genomics Institute
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Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Wdall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. an
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/clone="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
/cnote="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80
                                                                                                                                                                                                   /dev_stage="_3 to +3 DPA"
/lab_host="DH10B"
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Score:

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Result
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-MODEL-frame+ p2n.model -DEV=xlh
-Q-fcgn2_1/USPTO_spool/US10690564/runat_19082005_172308_25317/app_query.fasta_1.455
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOODECL=0
-LOODEXT=0 -UNITS-bits -START=1 -END=-1 -MARIX-ablosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=US10690564 @CGN 1 1 69 @runat 19082005 172308 25317 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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seq length: 2000000000
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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Match Length DB
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-949-016-2081

US-09-949-016-722

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Sequence 17, Appl Sequence 20, Appl Sequence 21, Appl Sequence 18, Appl Sequence 1149, App Sequence 722, App Sequence 4604, Ap Sequence 4605, Ap Sequence 1750, Ap Sequence 1, Appl Sequence 3, Appli Sequence 3, Appli
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ALIGNMENTS

US-09-325-932A-17

Sequence 17, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:

RESULT 1

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 17
LENGTH: 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                                                                                                                                               No.:
21 ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis
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                                                                          1 MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu
                                                        ATGTCGACTCTCACCGTCCCGCAGCCACTGCCCCCTGTAGCCGATGACTGCGAGCAGCTC
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Conservative:
Mismatches:
Indels:
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Sequence 20, Application US/09325932A

Patent NO. 6451604

(GENERAL INFORMATION:
APPLICANT: Plinn, Barry
APPLICANT: Lasham, Annette
TITILE OF INVENTION: Compositions affecting profile and their use in the FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 20
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; TYPE: DNA
; ORGANISM: Pinus 1
US-09-325-932A-20
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 Sequence 21, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification
FILE REFERENCE: 1022
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; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 21
; SEQ ID NO 21
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-21
Sequence 18, Application US/09325932A
Patent NO. 6451604
Patent NO. 6451604
Patent NO. 6451604
PAPPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
PITILE OF INVENTION: Compositions affecting pr
TITLE OF INVENTION: death and their use in th
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT APPLICATION NUMBER: US/09/325,932A
NUMBER OF SEQ ID NOS: 206
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US-09-325-932A-18
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN

TITLE OF INVENTION: WITH HUMAN DISEASE, ME

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEO ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2081
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US-09-949-016-2081
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LENGTH: 484
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ORGANISM: Pinus
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US-09-949-016-2081
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TYPE: DNA
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                                                                   ThrArgAlaGluIleAspLeuLysVallleGlyGluGluTyrGlnArgArgAsnSerIle
ProLeuGluLysAlaIleThrLysAspThrArgGlyAspTyrGluLysMetLeuValAla 310
                                                                                                                                                     LeuArgSerAlaIleAsnLysThrGlyThrAspGluGlyAlaLeuThrArgIleValThr
                                                                                                                                                                                                                       AlaLeuLeuArgSerThrIleGlnCysLeuThrArgProGluLeuTyrPheValAspVal
                                                                                                                                                                                                                                                                                                                              GAGATCCTGTGTTTAAGGAGCTTTCCTCAATTAAAACTAACATTTGATGAATACAGAAAT
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                                                 TCCÁGATCAGAAATTGÁCCTTTTGGACÁTTCGAACAGAGTTCAAGAAGCATTATGGCTAT
                                                                                                                     CTGCATCGAGCCTTGAAGGGTATTGGAACTGATGAGTTTACTCTGAACCGAATAATGGTG
                                                                                                                                                                                                                                                          ATCAGCCAAAAGGACATTGTGGACAGCATA---AAAGGAGAATTATCTGGGCATTTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGCAGATGGCAGAAGAGATGAAAGTCTGAAAGTGGATGAGCATCTGGCCAAACAAGAT
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Query Match:
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US-09-023-655-1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOLD PERFECT 6.1 for WI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERBWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilham
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ADDRESSEE: INCYTE PH
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                                                                                                                                                                                                                                                                                                                                  LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
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AAAATGCTCATCAGCATTCTGACTGAGAGGTCAAATGCACAGCGGCAGCTGATTGTTAAG
                             AspLeuIleIleSerIleLeuAlaHisArgSerAlaGluGlnArgLysValIleArgGln
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                                                                 AGCCCATCAGTGGATGCTGAAGCTATTCAGAAAGCAATCAGAAGGAATTGGAACTGATGAG
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                        RESULT 7
US-09-949-016-722
                                                                                                                                                                                                                    Sequence 722, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 722
LENGTH: 1339
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ORGANISM: Human
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                             ThrArgAlaGluIleAspLeuLysValIleGlyGluGluTyrGlnArgArgAsnSerIle :::|||:::||||
                                                                                                                                                                                                                                                                                        GAGATCCTGTGTTTAAGGAGCTTTCCTCAATTAAAACTAACATTTGAATAAAATACAGAAAT
                                                                                                                                                 GACTTACTGTTGGCCATAGTTAATTGTGTGAGGAACACGCCGGCCTTTTTAGCCGAAAGA
       TCCAGATCAGAAATTGACCTTTTGGACATTCGAACAGAGTTCAAGAAGCATTATGGCTAT
                                                                             CTGCATCGAGCCTTGAAGGGTATTGGAACTGATGAGTTTACTCTGAACCGAATAATGGTG
                                                                                                 LeuArgSerAlaIleAsnLysThrGlyThrAspGluGlyAlaLeuThrArgIleValThr
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                                                                                                                                                                                                                      ATCAGCCAAAAGGACÁTTGTGGACÁGCATA---AAAGGÁGAATTATCTGGGCATTTTGAA
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US-09-949-016-4604
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR TILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4604
LENGTH: 2386
TYPE: DNA
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Patent No. 6812339
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ValThrSerTyrArgTyrGluGlyAspGluValAsnMetThrLeuAlaLysGlnGluAla 172
                                                      LeuGluGluAspValAlaHisHisThrThrGlyAspPheArgLysLeuLeuValSerLeu
                                                                                                                                                                                                                                                   CTGGCAAGGCTGATTCTGGGGCTCATGATGCCACCGGCCCATTACGATGCCAAGCAGTTG 1357
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                                    CTGGAGGATGCTCTGAGCTCAGACACATCTGGCCACTTCAGGAGGATCCTCATTTCTCTG
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4605
LENGTH: 2386
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
TITLE OF INVENTION: WITH HUMAN DISEASE, N
FILE REFERENCE: CL001307
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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Matches:
Conservative:
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RESULT 10
US-09-949-016-1750
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                        Sequence 1750,
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DB:
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US-09-949-016-1750
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LENGTH: 1932
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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CLASSIFICATION: 435
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                                                                                                                     Sequence 3, Application US/08526136 Patent No. 6107089
                                                                                    GENERAL INFORMATION: APPLICANT: Towle,
                              NUMBER OF SEQUENCES: 3
                                                               TITLE OF INVENTION: ANNEXIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,665
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1070RMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
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                                                                                                                              AsnGluAlaThrLysArgTrpThrSerSerAsnGlnValLeuMetGluValAlaCysThr 112
                                                                                                                                                                                                                             PheGluArgAlaIleLeuLeuTrpThrLeuGluProGlyGluArgAspAlaLeuLeuAla
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LeuGluGluAspValAlaHisHisThrThrGlyAspPheArgLysLeuLeuValSerLeu 152
                                                                                           ArgThrSerThrGlnLeuLeuHisAlaArgGlnAlaTyrHisAlaArgTyrLysLysSer 132
                                                                                                                                                                                              TTTGAGAAGACAATCTTGGCCCTGATGAAGACCCCTGTCCTCTTTGACGCTTATGAGATA
                                                               CGCAGCAACGAGCACCCGGGAGCTGAACAGAGTCTACAAGACAGAATTCAAAAAGACC
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Matches:
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Percent Similarity:
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US-10-690-564-2 (1-317) x US-09-949-016-1199 (1-2054)
                                             Query Match:
DB:
                                                                                                                            Score:
                                                                                                                                                 Alignment Scores: Pred. No.:
                                                                                                                                                                                                           ) ORGANISM: Human US-09-949-016-1199
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN C.
TITLE OF INVENTION: WITH HUMAN DISEASE, MET
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                   SEQ ID NO 1199
LENGTH: 2054
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                    TYPE: DNA
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RESULT 14
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               Sequence 1200, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
 CURRENT APPLICATION
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NUMBER: US/09/949,016
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OF DETECTION AND USES THEREOF
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                    AspValAlaHisHisThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSer
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                                                                                                                                                                                                                                 TATCAAGCTGGTGAGGGGAGACTAGGGACCGATGAATCTTGCTTTAACATGATCCTTGCC
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                                                 AspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeuThrArgProGluLeuTyr 246
                                                                                                                                                                                             ThrArgSerLysAlaGlnIleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGlu
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR REPLICATION NUMBER: 60/237,768
PRIOR RELING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-949-016-1197
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1197, Application US/09949016 Patent No. 6812339
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ThrGlnLeuLeuHisAlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGlu :::::: ||||||:::
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                                                         ATGCAGGGAGCAGGAACTCAGGAACGTGTATTGAGTTGAGATTTTGTGCACAAGAACAAT
                                                                             ThrLysArgTrpThrSerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSer 115
                                                                                                                          CTGATCCTGGCCCTCTTCATGCCTCCTACGTATTACGATGCCTGGAGCTTACGGAAAGCA
                                                                                                                                                                                                TCCTATGGCAAGGATTTAATCAAAGATCTCAAATCAGAGTTAAGTGGAAATATGGAAGAA
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                                       307 MetLeuValAlaLeuLeuGlyGlu 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            872 CAGGAAATCCGAGAAATTGTCAGATGTTATCAGTCAGAATTTTGGACGAGACCTTGAAAAG 931
CTTCTTCTGGCTATTGTGGGCCAG 1468
                                                                                                            ArgAsnSerIleProLeuGluLysAlaIleThrLysAspThrArgGlyAspTyrGluLys 306
                                                                                                                                                                                     ArgIleValThrThrArgAlaGluIleAspLeuLysValIleGlyGluGluTyrGlnArg
                                                                                                                                                                                                                                                                  PheValAspValLeuArgSerAlaIleAsnLysThrGlyThrAspGluGlyAlaLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                     GACTTGTTAAGCAGTGTGAGCCGTGAGTTTTCCGGATATGTAGAAAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATCGTGATGAGAACCAGAGTATAAACCACCAAATGGCTCAGGAAGATGCTCAGCGTCTC 105:
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Search completed: August 22, 2005, 13:00:16 Job time: 275 secs

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-DB=PublIshed_Applications_NA -QFMT=fastap -SUFFTX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -STRAT=1 -END=-1 -MATRIX-blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100
-THR_MIN=0 -ALICW=15 -MODE-LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10690564_@CGN 1 480_@runat_19082005_172309_25406
-NCPU=6 -ICPU=3 -NO_MAAP -LARGEQUERY -NGS_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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seq length: 2000000000
Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

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26: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ORGANISM: Arabidopsis thaliana

TYPE: DNA

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                                         GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr
                                                                                      AspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysValIle
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yihuae
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5354)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 4242
LENGTH: 1184
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE: DNA
ORGANISM: Gossypium hirsutum
FEATURE: TANANA CAO.
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GENERAL INFORMATION:
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APPLICANT: Bloksberg, Leonard N.

ITITLE OF INVENTION: Materials and Methods for the

ITITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides

FILE REFERENCE: 11000.1012c3

CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: US 09/636,800

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: US 09/170,862

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: US 60/148,426

PRIOR APPLICATION NUMBER: US 60/148,426
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; ORGANISM: Eucalyptus
US-10-393-840-28
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Query Match:
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 28
LENGTH: 2588
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
                    NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7439
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 Sequence 7439, Application US/10425114
Publication No. US20040034888A1
                                                       TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28
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GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr
                                                                               ATCCGTCCCGAGAAGTACTTCGAGAAGGTTGTTCGCCTTGGCGATCAACAAGCGAGGAACC
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION OF SEQ ID NOS: 73128
SEQ ID NO 29928
LENGTH: 1145
TYPE: DNA
ORGANISM: Glycine max
FEATURE: Glycine max
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ACAACAGGAGACTTCCGTAAGCTCATACTACCTCTGGTTAGTTCTTATCGATATGAAGGA
                     ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
                                                                     GCGAGGAAGGCTTACCATGTTCTTTATAAGAAGTCTCTGGAGGAGGATGTTGCTCATCAC
                                                                                         AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
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RESULT 6
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; Publication No. US20040031072A1
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 1190
LENGTH: 1393
TYPE: DNA
CONTRACT CLASSICAL CANADAM CAN
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FEATURE:
OTHER INFORMATION: Clone
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            APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting projection of the project
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                                      AspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysValIle
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GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr
                                                                                               ThrArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThr
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CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/170,862
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR PPLICATION NUMBER: US 60/148,426
PRIOR PPLICATION NUMBER: US 70/148,426
PRIOR APPLICATION NUMBER: US 70/148,426
PRIOR FILING DATE: 1999-08-11
PRIOR PILING DATE: 1999-10-08
NUMBER OF SEO ID NOS: 956
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LENGTH: 1293
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APPLICANT: Bloksberg, Leonard N.
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; ORGANISM: Eucalyptus
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modificatic
FILE REFERENCE: 11000.102c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,
PRIOR FILING DATE: 1999-06-04
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Publication No. US20040034888A1
GENERAL INFORMATION:
            APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
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   APPLICATION NUMBER: US/10/425,114
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Best Local Similarity:
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; OTHER INFORMATION: Clone
US-10-425-114-10772
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NUMBER OF SEQ ID NOS: 7
SEQ ID NO 10772
LENGTH: 1145
TYPE: DNA
ORGANISM: Glycine max
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hrAspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysValI
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US-10-424-599-70457
US-10-424-599-70457
Sequence 70457, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecul
TITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 70457
LENGTH: 1321
Type: Nun
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Matches:
Conservative:
Mismatches:
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APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Wessener, Jeffrey P.
APPLICANT: Wessener, Jeffrey P.
APPLICANT: Garcia, Carlos A.
APPLICANT: Garcia, Carlos A.
APPLICANT: Slader, Ted
APPLICANT: Slader, Ted
APPLICANT: Allen, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT PILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 05/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
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US-09-770-149-655
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; SOFTWARE: FastSEQ for W
; SEQ ID NO 655
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Arabidopsis t
US-09-770-149-655
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Patent No. US20020059663A1
GENERAL INFORMATION:
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
Yu, Yang
Rameaka, Joshua G.
Page, Amy
Matthew, Abraham V.
Ladford, Brocket V.
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US-10-767-701-13525

US-10-767-701-13525, Application US/10767701

Sequence 13525, Application US-107684A1

Publication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated (TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 13525
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Pred. No.:
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Best Local Similarity:
Query Match:
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LENGTH: 1385
TYPE: DNA
ORGANISM: Sorghum bicolor
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GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr
                                                ---AAGGCTGACCCCAAGGATGAGTACCTCAAAACACTGCGGGCAATCATCCGGTGCTTC
                                                                                                                                                                                                                                                                                                                AspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys
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                                                                                                  AGTTGCCCCGACAGGTACTTTGAGAAGGTCGCCAGGCAGACATAGCGGGGCTAGGCACA
                                                                                                                     ThrArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThr
                                                                                                                                                                         GluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeu
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US-10-425-114-21986
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SEQ ID NO 21986
LENGTH: 1235
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Publication No. US20040034888A1
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
APPLICANT: Screen, Stev
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CURRENT FILING DATE: 2003-04-28
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
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ORGANISM: Zea mays
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
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                                                                                                  ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
                                                                                                                                                                                             AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
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AspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-425-114-26803
; Sequence 26803, Application US/10425114
; Publication No. US20040034888A1
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OTHER INFORMATION: Clone
US-10-425-114-26803
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26803
LENGTH: 1285
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ArgGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAsp
                                               AAGGAGGCGTACCAGAAGAGGAACAGCGTGCCGCTGGAGCGGGCCGTCGCGGGGGACACC
                                                                 GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr
                                                                                                            GATGAGAACTCCCTGACCAGGGTCATCACCACCCGCGCTGAGGTGGACCTCAAACTGATT
                                                                                                                                 AspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysValIle
                                                                                                                                                                        ThrArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThr
                                                                                                                                                                                                                                                               GluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeu
                                                                                                                                                                                                                                                                                                     CTGATTGCTACATTCAATCATTACAATGATGCATTTGGCCACCGAATCAACAAGGATCTG
                                                                                                                                                                                                                                                                                                                         IleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGluGluIleLeuLysSerLeu
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                                                                                                                                                                                                                                                                                                                                                               AspLysHisTyrAsnAspGluAspValIleArgIleLeuSerThrArgSerLysAlaGln
                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGAGGTCAACACAAGGTTGGCACACTCAGAAGCCAAACTACTTCATGAGAAGATCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCACTGGGGACTTCCGCAAGCTATTGGTGCCACTTGTAAGTACTTACCGCTATGATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuLeuLy8ThrLeuAspLy8GluLeuSerAsnAspPheGluArgAlaIleLeuLeuTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CECCACECCECECACCECCCATCCECCCCTTACECCGAEGCCTACEECGAEGAE
                                                                                                                                                                                                                                        --- AAGGCTGACCCCCAGGACGAGTACCTCAGAACGCTGCGGGCGATCATCCGGTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCAGGCAGGCTTATCACGAGCGGTTCAAGCGCTCGCTTGAGGAAGACATCGCTGCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCGGGAACCGTGTGCTCGAGATCGCCTGCACGCGCACCTCCGCGCAGATCTTCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCTCCGCTCCATCACGGACGAGATCTCCGGCGACTTCGAGAGGGCCGTGATCCTGTGG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgSerAlaGluGlnArgLysVallleArgGlnAlaTyrHisGluThrTyrGlyGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGCTGGACCCAGCGGAGCGCGACGCGGTGCTGGCCAACGAGGCGGCGCGCGGAAGTGGAAG
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